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OM nucleic - nucleic search, using sw model

Run on: July 11, 2003, 00:12:01 ; Search time 236 Seconds

(Without alignments)
3463.879 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363
Sequence: 1 caggttaccctgaagagtc.....ccctcagtcacccctcctca 363

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313.4	86.3	483	16	AA083491
2	313.4	86.3	483	20	AA083491
3	313.4	86.3	483	20	AA083491
4	311.8	85.9	423	16	AA083492
5	311.8	85.9	423	20	AA083492
6	311.8	85.9	423	20	AA083492
7	303.6	83.6	366	15	AA068709
8	299.2	82.4	738	15	AA070612
9	296.4	81.7	360	17	AA0709300

10	296.4	81.7	417	17	AA0709299
11	291	80.2	418	16	AA075889
12	282	77.7	1413	21	ABK11000
13	269	74.1	354	21	AA014500
14	267	73.6	369	21	AA099646
15	261.8	72.1	429	15	AA064166
16	250.8	69.1	812	14	AA037056
17	250.8	69.1	812	20	AA099479
18	250.8	69.1	812	21	AA051000
19	249.2	68.7	812	15	AA054437
20	195.8	53.9	363	22	AA042390
21	191.4	52.7	423	14	AA045597
22	191.4	52.7	423	20	AA039427
23	191.4	52.7	423	20	AA039427
24	190.6	52.5	423	20	AA079207
25	190.2	52.4	613	16	AA078943
26	185.4	51.1	418	16	AA075916
27	185.4	51.1	1607	22	AA066519
28	184.6	50.9	444	18	AA080181
29	183.8	50.6	418	16	AA075917
30	181.2	49.9	546	16	AA078964
31	181	49.9	437	21	AA042289
32	180.2	49.6	397	22	AA080854
33	179.8	49.5	400	21	AA000033
34	172.6	47.5	630	16	AA078948
35	171	47.1	423	16	AA083493
36	171	47.1	423	20	AA085887
37	171	47.1	423	20	AA079516
38	168.8	46.5	447	20	AA020406
39	168.4	46.4	646	24	ABR39075
40	165	45.5	714	18	AA086310
41	165	45.5	714	24	ABR92027
42	165	45.5	1173	18	AA086312
43	163.2	45.0	378	18	AA061237
44	163.2	45.0	1428	18	AA061279
45	162	44.6	477	20	AA020408

ALIGNMENTS

RESULT 1	AA083491	standard; cDNA; 483 BP.
ID	AA083491	
XX	AA083491	
AC	20-SEP-1995	(first entry)
XX		
DT		
XX		
DE	Mouse MAB 3B9 heavy chain.	
XX		
KW	Chimeric antibody; humanized antibody; antibody engineering;	
KW	monoclonal antibody; MAB; interleukin-4; IL-4; allergy; ds.	
XX		
OS	Mus sp.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	64..483
FT		/*tag- a
FT	sig-peptide	64..120
FT		/*tag- b
FT	mat-peptide	121..483
FT		/*tag- c
XX		
PN	W09507301-A.	
XX		
PD	16-MAR-1995.	
XX		
PF	07-SEP-1994;	94WO-US10308.
XX		
PR	07-SEP-1993;	93US-0117366.
PR	14-OCT-1993;	93US-0136783.
XX		

Murine anti-Protein heavy chain
DNA encoding prote
DNA sequence #1 in
Mouse antibody 136
Sequence of mouse
Rat immunoglobulin
KM50 Rat immunoglob
Rat activated immu
KM50 cell-derived
Nucleotide sequenc
Sequence encoding
Antibody B17X2 VH
Human B17X2 antibo
Anti-HIV-1 gp120 a
Human immunoglobul
Anti-human IL-6 ch
Human immune syste
Monoclonal antibod
Anti-human IL-6 ch
Human immunoglobul
Human 5' EST Isola
Human anti-HIV gpl
Human secreted pro
Human immunoglobul
Humanized antibody
Heavy chain variab
Heavy chain coding
IgG antibody 2.4.4
cDNA encoding lung
Single chain anti-
Anti-disialosyl
Single chain anti-
Human anti-RSV mon
Human anti-RSV mon
IgG antibody 2.3.2

PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI: 1995-123387/16.
 DR P-PSDB: AAR70190.
 XX
 XX Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
 PT from high affinity mabs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure: Fig. 2; 97pp: English.
 XX
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. CDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEMT+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AA083490-91), and used for
 CC antibody engineering.

Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

Query Match 86.3%; Score 313.4; DB 16; Length 483;
 Best Local Similarity 91.5%; Pred. No. 1.8e-86;
 Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 1 CAGGTTACTGTGAAGAAGTCTGGCCCTGGGATATTGAGACCCCTCCAGACCTCTAGTCTG 60
 DB 121 CAGGTTACTGTGAAGAAGTCTGGCCCTGGGATATTGAGACCCCTCCAGACCTCTAGTCTG 180
 OY 61 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTAGCTGGATTGCA 120
 DB 181 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTAGCTGGATTGCA 240
 OY 121 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTACTGATGATGACAGCCG 180
 DB 241 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTACTGATGATGACAGCCG 300
 OY 181 TATTAACCATCCCTGAAGAGCCGCTTACATCTCCAAAGGATATCTCCAGCAACAGTA 240
 DB 301 TATTAACCATCCCTGAAGAGCCGCTTACATCTCCAAAGGATATCTCCAGCAACAGTA 360
 OY 241 TTCTCTCAAGATCACCACTGTGGACATCGAGATACCTCCACATCTACTGTCTGGAAG 300
 DB 361 TTCTCTCAAGATCACCACTGTGGACATCGAGATACCTCCACATCTACTGTCTGGAAG 420
 OY 301 GTCTCTTACTGCTTATGCTATGACTACTGGGGTCAAGGAACCTAGTCACCGTCTCC 360
 DB 421 GAGACTGTCTTACTGCTTATGCTATGACTACTGGGGTCAAGGAACCTAGTCACCGTCTCC 480
 OY 361 TCA 363
 DB 481 TCA 483

RESULT 2
 AAX85885
 ID AAX85885 standard; CDNA: 483 BP.

AC AAX85885;

DT 13-SEP-1999 (first entry)

XX Heavy chain variable region CDNA of murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;

KM chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

KM immunoglobulin E-mediated allergic reaction; allergic rhinitis;

KM conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

KM rheumatoid arthritis; host-versus-graft disease; renal disease;

XX allergy; ds.

OS Mus sp.
 XX
 PN US928904-A.
 XX
 XX 27-JUL-1999.
 PD
 XX
 XX 07-JUN-1995; 95US-0483632.
 PF
 XX
 PR 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-0510308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI: 1999-429500/36.
 DR P-PSDB: AAY23768.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 PS Claim 3; Fig 2; 50pp; English.

CC The present sequence encodes the heavy chain variable region of
 CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.
 CC The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.

Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

Query Match 86.3%; Score 313.4; DB 20; Length 483;
 Best Local Similarity 91.5%; Pred. No. 1.8e-86;
 Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 1 CAGGTTACTGTGAAGAAGTCTGGCCCTGGGATATTGAGACCCCTCCAGACCTCTAGTCTG 60
 DB 121 CAGGTTACTGTGAAGAAGTCTGGCCCTGGGATATTGAGACCCCTCCAGACCTCTAGTCTG 180
 OY 61 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTAGCTGGATTGCA 120
 DB 181 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTAGCTGGATTGCA 240
 OY 121 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTACTGATGATGACAGCCG 180
 DB 241 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTACTGATGATGACAGCCG 300
 OY 181 TATTAACCATCCCTGAAGAGCCGCTTACATCTCCAAAGGATATCTCCAGCAACAGTA 240
 DB 301 TATTAACCATCCCTGAAGAGCCGCTTACATCTCCAAAGGATATCTCCAGCAACAGTA 360
 OY 241 TTCTCTCAAGATCACCACTGTGGACATCGAGATACCTCCACATCTACTGTCTGGAAG 300
 DB 361 TTCTCTCAAGATCACCACTGTGGACATCGAGATACCTCCACATCTACTGTCTGGAAG 420
 OY 301 GTCTCTTACTGCTTATGCTATGACTACTGGGGTCAAGGAACCTAGTCACCGTCTCC 360
 DB 421 GAGACTGTCTTACTGCTTATGCTATGACTACTGGGGTCAAGGAACCTAGTCACCGTCTCC 480
 OY 361 TCA 363
 DB 481 TCA 483

XX	AAAT9520	standard; cDNA; 483 bp.
XX	AAAT9520;	
XX	11-AUG-1999	(first entry)
XX	Heavy chain coding sequence for murine 3B9 antibody.	
XX	Antibody; interleukin-4; IL4; immunoglobulin E; Ige mediated disease;	
XX	allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;	
XX	atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;	
XX	autoimmune disease; graft versus host disease; ss.	
XX	Mus sp.	
XX	US914110-A.	
XX	22-JUN-1999.	
XX	07-JUN-1995;	95US-0483636.
XX	07-JUN-1995;	95US-0483636.
XX	07-SEP-1993;	93US-0117366.
XX	14-OCT-1993;	93US-0136783.
XX	07-SEP-1994;	94WO-0510308.
XX	(SMIK) SMITHKLINE BEECHAM CORP.	
XX	(SMIK) SMITHKLINE BEECHAM PLC.	
XX	Gross MS, Holmes SD, Sylvester DR;	
XX	WPI; 1999-370482/31.	
XX	P-PsDB; AAY18121.	
XX	Recombinant IL4 antibodies	
XX	Disclosure; Fig 2; 50pp; English.	
XX	This sequence encodes the heavy chain of the murine 3B9	
XX	antibody of the invention. The antibody is a chimeric or	
XX	humanised interleukin-4 (IL4) monoclonal antibody for the treatment of	
XX	immunoglobulin E (Ige) mediated diseases. The antibodies are useful for	
XX	the treatment of allergic disorders such as allergic rhinitis,	
XX	conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.	
XX	The antibodies are also useful for regulating B and T cell proliferation	
XX	and as such are useful in the treatment of autoimmune diseases and graft	
XX	versus host disease.	
XX	Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;	
XX	Query Match	86.3%; Score 313.4; DB 20; Length 483;
XX	Best Local Similarity	91.5%; Pred. No. 1.8e-86;
XX	Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0	
XX	1 CAGGTACTCTGAAAGAGCTGCGCCCTGGGATATTCGACCCCTCCAGACCTCACTG	60
XX	121 CAGGTACTCTGAAAGAGCTGCGCCCTGGGATATTCGACCCCTCCAGACCTCACTG	180
XX	61 ACTGTCTCTTCTCTGCGGTTTTCACCTGAGCACTTTCGTATGCGGTGAGCTGATTCGA	120
XX	181 ACTGTCTCTTCTCTGCGGTTTTCACCTGAGCACTTTCGTATGCGGTGAGCTGATTCGT	240
XX	121 CAGCCTTACAGAAAGAGCTGAGTGGCGTGGGACACATTTACTTGGGATATGCAAGGCG	180
XX	241 CAGCCTTACAGAAAGAGCTGAGTGGCGTGGGACACATTTACTTGGGATATGCAAGGCG	300
XX	181 TATAACCATCCCTGAGAGCGCGGTTACATATCTCCAAAGATACCTCCAGCAACGAGTA	240
XX	301 TATAACCATCCCTGAGAGCGCGGTTACATATCTCCAAAGATACCTCCAGCAACGAGTA	360
XX	241 TTCTCAAGATACCAAGTGTGGACACTGCAGATTAATCTACTGCTGCTGGAAG	300

DB	361	TTCCCAAGATCACCAGTGTGGACACTGCAGTACTGCACACTACTACTGTCTGCAGA	420
OY	301	GTCTCTCTACTGCTATGCTATGACACTACTGGGTCAGAAGACCTCACTCACCCTTCC	360
DB	421	GAGACTGTGTCTACTGGTACTGCATGTCTGGGGCGGAGGACCGCTCACCGTCTCC	480
OY	361	TCA 363	
DB	481	TCA 483	
RESULT 4			
AA083492	ID	AA083492 standard; cDNA; 423 BP.	
XX	AC	AA083492;	
XX	DT	20-SEP-1995 (first entry)	
XX	DE	Chimeric antibody 3B9 heavy chain.	
XX	KW	Chimeric antibody; antibody engineering; monoclonal antibody;	
XX	MA	MAB; Interleukin-4; IL-4; allergy; ds.	
XX	OS	Homo sapiens; Mus sp.	
XX	FH	Key	
XX	FT	CDS	
XX	FT	Location/Qualifiers	
XX	FT	1..423	
XX	FT	/*tag- a	
XX	FT	sig_peptide	
XX	FT	1..57	
XX	FT	/*tag- b	
XX	FT	mat_peptide	
XX	FT	58..423	
XX	FT	/*tag- c	
XX	PN	W09507301-A.	
XX	PD	16-MAR-1995.	
XX	PF	07-SEP-1994; 94MO-US10308.	
XX	PR	07-SEP-1993; 93US-0117366.	
XX	PR	14-OCT-1993; 93US-0136783.	
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX	PA	(SMIK) SMITHKLINE BEECHAM PLC.	
XX	PI	Gross MS, Holmes SD, Sylvester DR;	
XX	DR	WPI; 1995-123387/16.	
XX	DR	P-PSDB; AAR70191.	
XX	PT	Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived	
XX	PT	from high affinity mabs - useful in treatment of IL-4-mediated	
XX	PT	and IgE-mediated allergic conditions	
XX	PS	Disclosure; Fig.3; 97pp; English.	
XX	CC	A human/mouse chimeric antibody heavy chain variable region was	
XX	CC	constructed (given in AAR70191) that contained the mouse anti-human	
XX	CC	IL-4 MAb 3B9 variable region including 3 CDRs (AAR70198-200) and a	
XX	CC	human antibody signal peptide (AAR70193). The construct was used	
XX	CC	for humanized antibody production.	
XX	SC	Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;	
OY	Query Match	85.9%; Score 311.8; DB 16; Length 423;	
OY	Best Local Similarity	91.2%; Pred. No. 5,4e-86;	
OY	Matches 331; Conservative	0; Mismatches 32; Indels 0; Gaps 0	
DB	1	CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATGACAGCCCTCCAGACCTCAGTCTG	60
DB	61	CAGTTTACCTTGAAGAAGTCTGGCCCTGGGATATGACAGCCCTCCAGACCTCAGTCTG	120

QY 61 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTGCA 120
 DB 121 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTGCT 180
 QY 121 CAGCTTCAGGAAAGGCTCTGAGAGTGGCTGGACACATTTTACTGGATGATGACAGCC 180
 DB 181 CAGCTTCAGGAAAGGCTCTGAGAGTGGCTGGACACATTTTACTGGATGATGACAGCC 240
 QY 181 TATACCCATCCCTGAGAGCGGCTTACATCTCCAGAGTACTCCAGACACAGTA 240
 DB 241 TATACCCATCCCTGAGAGCGGCTTACATCTCCAGAGTACTCCAGACACAGTA 300
 QY 241 TTCCTCAAGATCACCAGTGTGACACATCTGAGATCTCCATCTACTGTCTGGAAG 300
 DB 301 TTCCTCAAGATCACCAGTGTGACACATCTGAGATCTCCATCTACTGTCTGGAAG 360
 QY 301 GTCTCTTACTGCTTACTGCTATGAGTACTGAGGTCAAGAACCTTACCTGCTCC 360
 DB 361 GAGACTGTGTCTACTGCTATGATGTCTGGGGCCAGGACGACGTCACCGTCTCC 420
 DB 421 TCA 423
 RESULT 5
 ID AAX85886 standard; cDNA; 423 BP.
 AC AAX85886:
 DT 13-SEP-1999 (first entry)
 DE Heavy chain variable region cDNA of murine/human chimeric antibody 3B9.
 XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; ds.
 XX Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX US5928904-A.
 PN 27-JUL-1999.
 XX 07-JUN-1995; 95US-0483632.
 PR 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX PI Gross MS, Holmes SD, Sylvester DR;
 XX WPI: 1999-429500/36.
 DR P-PSDB: AAY23769.
 XX New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 XX Example 3; Fig 3; 50pp; English.
 PS The present sequence encodes the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal

CC antibodies. The antibodies of the invention are used in therapeutic
 CC and pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 XX Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
 SO
 Query Match 85.98; Score 311.8; DB 20; Length 423;
 Best Local Similarity 91.28; Pred. No. 5.4e-86;
 Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 1 CAGGTTACTGCGAAAGAGTCTGGGCTGGGATATGAGCCCTCCAGACCTCAGTCTG 60
 DB 61 CAGGTTACTGCGAAAGAGTCTGGGCTGGGATATGAGCCCTCCAGACCTCAGTCTG 120
 QY 61 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTGCA 120
 DB 121 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTGCT 180
 QY 121 CAGCTTCAGGAAAGGCTCTGAGAGTGGCTGGACACATTTTACTGGATGATGACAGCC 180
 DB 181 CAGCTTCAGGAAAGGCTCTGAGAGTGGCTGGACACATTTTACTGGATGATGACAGCC 240
 QY 181 TATACCCATCCCTGAGAGCGGCTTACATCTCCAGAGTACTCCAGACACAGTA 240
 DB 241 TATACCCATCCCTGAGAGCGGCTTACATCTCCAGAGTACTCCAGACACAGTA 300
 QY 241 TTCCTCAAGATCACCAGTGTGACACATCTGAGATCTCCATCTACTGTCTGGAAG 300
 DB 301 TTCCTCAAGATCACCAGTGTGACACATCTGAGATCTCCATCTACTGTCTGGAAG 360
 QY 301 GTCTCTTACTGCTTACTGCTATGAGTACTGAGGTCAAGAACCTTACCTGCTCC 360
 DB 361 GAGACTGTGTCTACTGCTATGATGTCTGGGGCCAGGACGACGTCACCGTCTCC 420
 QY 361 TCA 363
 DB 421 TCA 423
 RESULT 6
 ID AAX79542 standard; cDNA; 423 BP.
 AC AAX79542:
 DT 11-AUG-1999 (first entry)
 DE Chimeric 3B9 monoclonal antibody heavy chain coding sequence.
 XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease; ss.
 XX Synthetic.
 OS US5914110-A.
 PN 22-JUN-1999.
 XX 07-JUN-1995; 95US-0483636.
 PR 07-JUN-1995; 95US-0483636.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI: 1999-370482/31.

DR P-PSDB: AAY18125.

XX Recombinant IL4 antibodies

XX Example 5; Fig 3; 50pp; English.

CC This sequence represents the DNA encoding the light chain of the
CC chimeric 3B9 antibody of the invention. The antibody is a chimeric or
CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
CC the treatment of allergic disorders such as allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
CC The antibodies are also useful for regulating B and T cell proliferation
CC and as such are useful in the treatment of autoimmune diseases and graft
CC versus host disease.

SO Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;

Query Match 85.9%; Score 311.8; DB 20; Length 423;

Best Local Similarity 91.2%; Pred. No. 5.4e-86;

Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 60

DB 61 CAGGTTACCCCTGAAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 120

QY 61 ACTGTTCTCTCTCTGGGTTTCACTAGACACTTCTGGTATGGGTTGAGCTGGATTGCA 120

DB 121 ACTGTTCTCTCTCTGGGTTTCACTAGACACTTCTGGTATGGGTTGAGCTGGATTGCA 180

QY 121 CAGGCTTCAGAAAGAGTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 180

DB 181 CAGGCTTCAGAAAGAGTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 240

QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGAACAGGTA 240

DB 241 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGAACAGGTA 300

QY 241 TTCCTCAAGATCACCAGTGTGACACATCGAGATAGTGCACATACTACTGTGCTGAAG 300

DB 301 TTCCTCAAGATCACCAGTGTGACACATCGAGATAGTGCACATACTACTGTGCTGAAG 360

QY 301 GTCTCTTAACTGCTATGCTATGACTACTGGGGTCAAGACCTCAGTACCGCTCC 360

DB 361 GAGACTGTGTTCTACTGTTACTGATGTCTGGGGCGGACGACGATCAGCTCC 420

QY 361 TCA 363

DB 421 TCA 423

RESULT 7

AA068709 standard; cDNA to mRNA; 366 BP.

XX AA068709;

XX 08-FEB-1995 (first entry)

XX Humanised Mab H-chain coding sequence.

XX Human; mouse; murine; heavy; light; chain; monoclonal; antibody;

XX complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN; ds.

XX Chimeric - Mus musculus.

XX Chimeric - Homo sapiens.

XX JP06141885-A.

XX 24-MAY-1994.

XX 05-NOV-1992; 92JP-0322476.

XX 05-NOV-1992; 92JP-0322476.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKUYUSHO.

XX WPI: 1994-205040/25.

DR P-PSDB: AAR54101.

XX Recombinant anti-HIV monoclonal antibody - capable of

XX neutralising strains which can not be neutralised by anti-IIIB

XX and IIIMN antibodies

XX Disclosure; Page 13; 23pp; Japanese.

CC The sequences given in AA068709-10 encode the heavy and light chains
CC respectively of the humanised monoclonal antibody (Mab) of the
CC invention. The antibody has the ability to neutralise human
CC immunodeficiency virus. The antibody is classified as IgG kappa and
CC has the sequence RIGPR or RVGPR in the principal neutralising
CC domain. The antibody may be used to neutralise the clinically
CC separate strains which cannot be neutralised by the neutralising
CC antibodies against IIIB and IIIMN strains.

SO Sequence 366 BP; 85 A; 98 C; 84 G; 99 T; 0 other;

Query Match 83.6%; Score 303.6; DB 15; Length 366;

Best Local Similarity 91.3%; Pred. No. 1.7e-83;

Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 60

DB 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 60

QY 61 ACTGTTCTCTCTCTGGGTTTCACTAGACACTTCTGGTATGGGTTGAGCTGGATTGCA 120

DB 61 ACCGTTCTCTCTCTGGGTTTCACTAGACACTTCTGGTATGGGTTGAGCTGGATTGCA 120

QY 121 CAGGCTTCAGAAAGAGTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 180

DB 121 CAGGCTTCAGAAAGAGTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 180

QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGAACAGGTA 240

DB 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGAACAGGTA 240

QY 241 TTCCTCAAGATCACCAGTGTGACACATCGAGATAGTGCACATACTACTGTGCTGAAG 300

DB 241 TTCCTCAAGATCACCAGTGTGACACATCGAGATAGTGCACATACTACTGTGCTGAAG 300

QY 301 G--TCTCTTAACTGCTATGCTATGACTACTGGGGTCAAGACCTCAGTACCGCTC 357

DB 301 GTCTCTATGTTAACTCGATTATGACACATCGGGGTCAAGACCTCAGTACCGCTC 360

QY 358 TCCTCA 363

DB 361 TCCTCA 366

RESULT 8

AA070612 standard; DNA; 738 BP.

XX AA070612;

XX 28-APR-1995 (first entry)

XX IL-6 binding inhibitor DNA.

XX Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;

KW septic shock; multiple myeloma; ss.
 XX Homo sapiens.
 XX EPI17126-A.
 XX 28-SEP-1994.
 XX 16-FEB-1994; 94EP-0102346.
 XX 17-FEB-1993; 93JP-0028173.
 XX (AJIN) AJINOMOTO KK.
 XX Hamuro J, Nakazawa H, Shimamura T;
 XX WPI: 1994-295777/37.
 XX P-PSDB: AAR58612.
 DR Polypeptide inhibiting binding of human interleukin-6 (IL-6) to
 PT its receptor - useful for treating auto-immune disease induced
 PS or aggravated by IL-6
 PS Claim 9; Page 19; 26pp; English.
 CC AAG70612 codes for human interleukin-6 binding inhibitor, the
 CC polypeptide described in AAR58612. This polypeptide inhibits the
 CC binding of human IL-6 to its receptor, and can therefore be
 CC useful in the treatment of a variety of autoimmune diseases;
 CC specifically in the treatment of rheumatoid arthritis, septic
 CC shock due to bacterial infection and multiple myeloma.
 XX
 SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T; 0 other;
 Query Match 82.4%; Score 299.2; DB 15; Length 738;
 Best Local Similarity 90.1%; Pred. No. 4.9e-82;
 Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;
 QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60
 DB 367 CAGGTCAAACTCGAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 426
 QY 61 ACTTGTCTTCTCTCTGGTTTCTACTGACACTTCTGTATGGGTGAGCTGATTGCA 120
 DB 427 ACTTGTCTTCTCTCTGGTTTCTACTGACACTTCTGTATGGGTGAGCTGATTGCT 486
 QY 121 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 180
 DB 487 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 546
 DB 181 TATTAACCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
 DB 547 TATTAACCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 606
 QY 241 TTCTCTAAGATCAGCACTGTGGACATCGAGATCTCCACATCTCTGTGCTCGAAG- 299
 DB 607 TTCTCTAAGATCAGCACTGTGGACATCGAGATCTCCACATCTCTGTGCTCGAAG- 666
 QY 300 -----GGTCTCTTAACCTATGCTATGAGTACTGAGGCTCAAGAACTCTAGTC 351
 DB 667 AGTCTATAGTATTTGGGGGAGCTATGCTATGAGTACTGAGGCTCAAGAACTCTAGTC 726
 QY 352 ACCGTCCTCA 363
 DB 727 ACCGTCCTCA 738
 RESULT 9
 AAT09300
 ID AAT09300 standard; DNA: 360 BP.
 XX
 AC AAT09300;
 XX

DT 25-JUL-1996 (first entry)
 XX
 DE Murine anti-protein C MAb HPC-4 VH gamma mature protein coding region.
 XX
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
 XX
 OS Mus musculus.
 XX
 FN W09534652-A1.
 XX
 PD 21-DEC-1995.
 XX
 PE 09-JUN-1995; 95WO-US07372.
 XX
 PR 10-JUN-1994; 94US-0259321.
 XX
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 XX
 PI Esmon CT, Rezaie A;
 XX
 DR WPI: 1996-049681/05.
 XX
 DR P-PSDB: AAR8109.
 XX
 PT Calcium-binding monoclonal antibody immunoreactive with protein C -
 PT inhibits protein C anticoagulant activation by
 PS thrombin-thrombomodulin, e.g. for treating tumours
 PS Claim 4; Page 30; 41pp; English.
 XX
 CC This is the nucleotide sequence encoding the mature protein from the
 CC murine anti-protein C monoclonal antibody HPC-4 heavy chain variable
 CC region (VH gamma). HPC-4 recognises the activation peptide region
 CC (AAR8106) of the heavy chain of protein C, a vitamin K-dependent plasma
 CC protein zymogen. Protein C is activated to activated protein C (APC)
 CC by cleavage between the Arg-Leu amino acid contained within the
 CC activation peptide sequence. HPC-4 prevents protein C activation to
 CC APC by binding to this region. The DNA sequences encoding the variable
 CC regions of the heavy and light chains of the antibody (AAT09299-302)
 CC were used to construct humanised antibodies using the PCR primers
 CC AAT09303-9. The humanised antibodies are useful as inhibitors of
 CC coagulation and can be used for the treatment of tumours by inhibiting
 CC the anticoagulant activity of APC by preventing conversion of protein C
 CC to APC.
 XX
 SQ Sequence 360 BP; 82 A; 91 C; 95 G; 92 T; 0 other;
 Query Match 81.7%; Score 296.4; DB 17; Length 360;
 Best Local Similarity 90.6%; Pred. No. 2.8e-81;
 Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
 QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60
 DB 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60
 QY 61 ACTTGTCTCTCTCTGGTTTCTACTGACACTTCTGTATGGGTGAGCTGATTGCA 120
 DB 61 ACTTGTCTCTCTCTGGTTTCTACTGACACTTCTGTATGGGTGAGCTGATTGCT 120
 QY 121 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 180
 DB 121 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 180
 DB 181 TATTAACCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
 DB 181 TATTAACCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
 QY 241 TTCTCTAAGATCAGCACTGTGGACATCGAGATCTCCACATCTCTGTGCTCGAAG 300
 DB 241 TTCTCTAAGATCAGCACTGTGGACATCGAGATCTCCACATCTCTGTGCTCGAAG 300
 QY 301 GTCTCTTAACCTATGCTATGAGTACTGAGGCTCAAGAACTCTAGTCACCGTCTCC 360

DB 301 ATGAT---GATTAGACGCTATGACTACTGGGTCAGAGAACCTGACCGTCTCC 357
 QY 361 TC 362
 DB 358 TC 359

RESULT 10 AAT09299

ID AAT09299 standard; DNA; 417 BP.

AC AAT09299;

DT 25-JUL-1996 (first entry)

DE Murine anti-Protein C MAb HPC-4 VH gamma coding region.

XX Epitope: activation; heavy chain; protein C; vitamin K; plasma protein;
 XX zymogen; cleavage; mouse; humanised antibody; variable region;
 XX light chain; inhibition; anticoagulant; coagulation; tumour; ss.

OS Mus musculus.

XX Key Location/Qualifiers
 FH sig_peptide 1..57
 FT /*tag= a
 FT mat_peptide 58..417
 FT /*tag= b

XX W09534652-A1.

XX 21-DEC-1995.

XX 09-JUN-1995; 95WO-US07372.

XX 10-JUN-1994; 94US-0259321.

XX (OKLA-) OKLAHOMA MED RES FOUND.

XX Eamon CT, Rezaie A;

XX WPI; 1996-049681/05.

XX P-PSDB; AAR88107.

XX Calcium-binding monoclonal antibody immunoreactive with Protein C -
 XX inhibits Protein C anticoagulant activation by
 XX thrombin-thrombomodulin, e.g. for treating tumours

PS Claim 4; Page 29-30; 41pp; English.

XX This is the nucleotide sequence encoding the heavy chain variable region
 XX from the murine anti-protein C monoclonal antibody HPC-4 which
 XX recognises the activation peptide region (AAR88106) of the heavy chain of
 XX protein C, a vitamin K-dependent plasma protein zymogen. Protein C is
 XX converted to activated protein C (APC) by cleavage between the Arg-Lys
 XX amino acid contained within the activation peptide sequence. HPC-4
 XX sequences encoding the variable regions of the heavy and light chains of
 XX the antibody (AAT09299-302) were used to construct humanised antibodies
 XX using the PCR primers AAT09303-9. The humanised antibodies are useful as
 XX inhibitors of coagulation and can be used for the treatment of tumours by
 XX inhibiting the anticoagulant activity of APC by preventing conversion of
 XX protein C to APC.

XX Sequence 417 BP; 89 A; 108 C; 106 G; 114 T; 0 other;

XX Query Match 81.7%; Score 296.4; DB 17; Length 417;

XX Best Local Similarity 90.6%; Pred. No. 2.9e-81;

QY Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
 1 CAGGTTACTCTGAAGAAGCTGGCCCTGGATATTGACGCCCTCCAGACCCCTAGTCTG 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 58 CAGGTTACTCTGAAGAAGCTGGCCCTGGATATTGACGCCCTCCAGACCCCTAGTCTG 117
 QY 61 ACTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGTAATGGGTGACGTGATTCGA 120
 DB 118 ACTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGTAATGGGTGACGTGATTCGT 177
 QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGTGACACATTTTACTGGATGATGACAAAGCC 180
 DB 178 CAGCCTTCAGGAAGGGTCTGGAGTGGTGACACATTTTACTGGATGATGACAAAGCC 237
 QY 181 TATAACCCATCCCTGAAGAGCCGCTTACAATCTCCAGAGTACCTCCAGCAACAGTA 240
 DB 238 TATAACCCAGTCTGAAGAGCCGCTTACAATCTCCAGAGTACCTCCAGCAACAGTA 297
 QY 241 TTCCTCAAGATCACCAGTGTGACACTGACATFACCTGACATFACCTGCTCGAAG 300
 DB 298 TTCCTCAAGATCACCAGTGTGACACTGACATFACCTGACATFACCTGCTCGAATG 357
 QY 301 GTCCTCTAATGCTGATGCTATGAGTACTGAGGTCAGAGAACCTCAGTACCGTCTCC 360
 DB 358 ATGAT---GATTAGACGCTATGACTACTGGGTCAGAGAACCTCAGTACCGTCTCC 414
 QY 361 TC 362
 DB 415 TC 416

RESULT 11

ID AAT075889 standard; CDNA; 418 BP.

AC AAT075889;

DT 21-AUG-1995 (first entry)

DE Mouse heavy chain variable region in plasmid pUC-SK2-Vh.

XX Primer: PCR; amplify; kappa; light chain; variable region; mouse; human;
 XX interleukin; antibody; hybridoma; CDR; framework; constant region;
 XX heavy chain; disorder; antigenicity; ds.

OS Synthetic.

XX Key Location/Qualifiers
 FH CDS 1..417
 FT /*tag= a
 FT sig_peptide /product= mouse heavy chain variable region
 FT /*tag= b
 FT mat_peptide 58..417
 FT /*tag= c

XX W09428159-A.

XX 08-DEC-1994.

XX 30-MAY-1994; 94WO-JP00859.

XX 31-MAY-1993; 93JP-0129787.

XX (CHUS) CHUGAI SEIYAKU KK.

XX (CHUS) CHUGAI PHARM CO LTD.

XX Hirata Y, Sato K, Tsuchiya M;

XX WPI; 1995-022828/03.

XX P-PSDB; AAR67655.

XX Antibody against IL-6 - useful for the therapy and treatment of
 XX IL-6 related disorders.
 XX Claim 10; Page 49; 82pp; Japanese.

CC The sequence of the gene encoding the heavy chain variable region of
CC the mouse anti-human Interleukin-6 (IL-6) antibody. The fragment was
CC amplified by primers (AA075876-87) from cDNA derived from mRNA from
CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19
CC to produce plasmid pUC-SK2-VH. The inserted fragment is used to
CC generate constructs (see AA075914-7) encoding fragments of an antibody to
CC the human IL-6 comprising (a) a light chain with (1) a variable region
CC containing 3 complementarity determining regions (CDR) (AA07201-3)
CC inserted into several framework regions (FR) (AA07204-7) and (11) a human
CC light chain constant region and (b) a heavy chain with (1) a variable
CC region containing 3 CDR (AA072212-4) inserted into an FR (AA072215-8) and
CC (11) a human light chain constant region. The FR of the light chain may
CC be mouse derived (AA075888) or from the human antibody REI. The heavy
CC chain FR may also be mouse derived (AA075889) or from the human antibody
CC DMV. The antibodies can be used in the treatment of IL-6 related
CC disorders. The antibodies are useful as they have low antigenicity due to
CC the use of human derived sequences and low antigenicity mouse derived
CC sequences.

XX Sequence 418 BP; 96 A; 113 C; 99 G; 110 T; 0 other;

XX Query Match

Best Local Similarity 80.2%; Score 291; DB 16; Length 418;

XX Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTTACTGTGAAAGAGTGTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCACTCTG 60
DB 58 CAGGTTACTGTGAAAGAGTGTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCACTCTG 117
QY 61 ACTTGTCTTCTCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 118 ACTTGTCTTCTCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 177
QY 121 CAGGCTTCAAGAAAGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 178 CAGGCTTCAAGAAAGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
QY 181 TATTAACCATCCCTGAAAGAGCCGGCTTCAATCTCAAGATATCTCCAGCAACCAAGTA 240
DB 238 TATTAACCATCCCTGAAAGAGCCGGCTTCAATCTCAAGATATCTCCAGCAACCAAGTA 297
QY 241 TTTCTCAAGATCCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 298 TTTCTCAAGATCCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357
QY 301 GTCCTCTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 358 GAGGAT---TACGACGAAGCTATGAGTACTGCGGCTCAAGGAACCTCAGTCACCGTCTCC 414
361 TCA 363
415 TCA 417

RESULT 12

ID ABK11000 standard; DNA; 1413 BP.

XX ABK11000;

XX 06-JUN-2002 (first entry)

XX DNA encoding protein #2 in invention relating to von Willebrand factor.

XX Von Willebrand factor; gene; ds.

XX Unidentified.

XX Key Location/Qualifiers

XX FT CDS 1..1413

XX FT /product- "Protein #2"

XX XX

PN KR9006382-A.
XX 16-AUG-1999.
PD 24-JAN-1998; 98KR-0002265.
XX 24-JAN-1998; 98KR-0002265.
XX 24-JAN-1998; 98KR-0002265.
XX (GRC) KOREA GREEN CROSS CORP.
PI Kim HC, Kim JS, Byun TH, Lee JS, Oh HG, Lee JM, Kim BJ;
DR WPI: 2000-547436/50.
DR P-PSDB: AAU77289.
XX Method for purifying factor VIII using chimera antibody to von
XX Willebrand factor -
XX Disclosure; Fig 2; 12pp; Korean.

CC The present invention relates to von Willebrand factor. The present
CC sequence encoding a protein of unknown function is given in the
CC specification of the present invention.

XX Sequence 1413 BP; 326 A; 445 C; 373 G; 269 T; 0 other;

XX Query Match

Best Local Similarity 77.7%; Score 282; DB 21; Length 1413;

XX Matches 312; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 2 AGTGTACTGTGAAAGAGTGTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCACTCTG 61
DB 59 AGTGTACTGTGAAAGAGTGTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCACTCTG 118
QY 62 CTGCTCTCTCTCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
DB 119 CTGCTCTCTCTCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 178
QY 122 AGCCTTCAAGAAAGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
DB 179 AGCCTTCAAGAAAGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238
QY 182 ATTAACCATCCCTGAAAGAGCCGGCTTCAATCTCAAGATATCTCCAGCAACCAAGTA 241
DB 239 ATTAACCATCCCTGAAAGAGCCGGCTTCAATCTCAAGATATCTCCAGCAACCAAGTA 298
QY 242 TCCCTCAAGATCCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
DB 299 TCCCTCAAGATCCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 358
QY 302 TCTCTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
DB 359 GAAACAGGAGCGGAGCTGTGTTGCTTACTGCGGCTCAAGGAACCTCAGTCACCGTCTCC 418
362 CA 363
419 CA 420

RESULT 13

ID AAS14500 standard; DNA; 354 BP.

XX AAS14500;

XX 06-JUN-2002 (first entry)

XX DNA sequence #1 in invention relating to von Willebrand factor.

XX Von Willebrand factor; ds.

XX Unidentified.

XX XX

PN KR9906382-A.
 XX 16-AUG-1999.
 XX 24-JAN-1998; 98KR-0002265.
 XX 24-JAN-1998; 98KR-0002265.
 XX (GRC) KOREA GREEN CROSS CORP.
 PA Kim HC, Kim JS, Byun TH, Lee JS, Oh HG, Lee JM, Kim BJ;
 PI WPI: 2000-547436/50.
 DR Method for purifying factor VIII using chimera antibody to von
 PT Willebrand factor -
 XX Claim 5; Page 7; 12pp; Korean.
 The present invention relates to von Willebrand factor. The present
 CC DNA sequence of unknown function is given in the specification of
 the present invention.
 XX Sequence 354 BP; 76 A; 97 C; 98 G; 83 T; 0 other;

Query Match 74.1%; Score 269; DB 21; Length 354;
 Best Local Similarity 86.6%; Pred. No. 7.4e-73;
 Matches 309; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
 DB 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
 QY 61 ACTGTCTTCTCTCTGGGTTTACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120
 DB 61 ACTGTCTTCTCTCTGGGTTTACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120
 QY 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGACACATTTACGGGATGATGACAAAGCCG 180
 DB 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGACACATTTACGGGATGATGACAAAGCCG 177
 QY 181 TATACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGTACTCCAGCAACAGGTA 240
 DB 178 TATACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGTACTCCAGCAACAGGTA 237
 QY 241 TTCTCTCAAGTACACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 300
 DB 238 TTCTCTCAAGTACACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 297
 QY 301 GTCTCTCTTACCTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 357
 DB 298 GGAACAGGAGGAGGAGCTGCTGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354

RESULT 14
 ID AAA99646 standard; cDNA; 369 BP.
 XX AAA99646;
 AC
 XX 25-JAN-2001 (first entry)
 DE Mouse antibody 1369 heavy chain variable region cDNA.
 XX
 XX Mouse: antibody 1369; antiarthritic; immunosuppressive; neuroprotective;
 KW antiinflammatory; antiproliferative; interleukin-18; IL-18;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
 KW inflammatory bowel disease; complementarity determining region; CDR; ss.
 XX Mus musculus.
 OS
 XX
 FH Key Location/Qualifiers

FT CDS 1..369
 FT /tag- a
 FT /partial
 FT /product= "antibody 1369 heavy chain variable region"
 PN WO200056771-A1.
 XX 28-SEP-2000.
 XX 17-MAR-2000; 2000WO-US07349.
 XX 19-MAR-1999; 99US-0125299.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
 DR WPI: 2000-628249/60.
 DR P-PADB; AAB21367.

Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal
 PT antibody having high affinity and useful for treating IL-18 mediated
 PT disorders such as multiple sclerosis, rheumatoid arthritis and
 PT psoriasis -
 XX Claim 4; Fig 4; 64pp; English.
 The present sequence encodes the heavy chain variable region of the mouse
 CC antibody 1369. The antibody has high affinity for human interleukin-18
 CC (IL-18) and is useful for treating and diagnosing IL-18-mediated
 CC disorders, e.g. autoimmune diseases such as multiple sclerosis,
 CC rheumatoid arthritis, type I or insulin dependent diabetes, inflammatory
 CC bowel disease and psoriasis. Specific changes can be introduced
 CC into the nucleotide sequences encoding the complementarity determining
 CC regions (CDRs) or framework regions of the variable light chain and
 CC heavy chain peptides. The resulting modified or fusion nucleic acid
 CC sequences can then be introduced into a plasmid for expression.

Sequence 369 BP; 81 A; 96 C; 89 G; 103 T; 0 other;

Query Match 73.6%; Score 267; DB 21; Length 369;
 Best Local Similarity 84.8%; Pred. No. 3.1e-72;
 Matches 313; Conservative 0; Mismatches 50; Indels 6; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
 DB 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
 QY 61 ACTGTCTTCTCTCTGGGTTTACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120
 DB 61 ACTGTCTTCTCTCTGGGTTTACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120
 QY 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGACACATTTACGGGATGATGACAAAGCCG 180
 DB 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGACACATTTACGGGATGATGATTAAGTAT 180
 QY 181 TATACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGTACTCCAGCAACAGGTA 240
 DB 181 TATACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGTACTCCAGCAACAGGTA 240
 QY 241 TTCTCTCAAGTACACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 300
 DB 241 TTCTCTCAAGTACACAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 296
 QY 297 --AAGGCTCTCTTACCTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 354
 DB 301 CATTAGAGGAGTGTAGCTCTCTGCTATGAGTACTGAGGAGTCAAGAACTGATCACC 360
 QY 355 GTCTCTCA 363
 DB 361 GTCTCTCA 369

RESULT 15

AA064166 standard; cDNA to mRNA; 429 BP.

AA064166;

29-DEC-1994 (first entry)

Sequence of mouse VH showing the sequences of recombinant anti-FHV-1 antibody CDRs 1, 2 and 3.

Feline herpes virus; FHV-1; monoclonal antibody; CDR; complementarity determining region; ss.

Mus musculus.

Key Location/Qualifiers

1..429

misc_feature

/*tag= a

19

misc_feature

/*tag= b

/label= MHL341

misc_feature

385..429

/*tag= c

/label= MCH3

MO9412661-A.

09-JUN-1994.

25-NOV-1993; 93MO-JP01724.

28-NOV-1992; 92JP-0341255.

(KAGA) CHEMO SERO THERAPEUTIC RES INST.

Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

WPI; 1994-200288/24.

P-PSDB; AAR54092.

Feline monoclonal antibody and recombinant antibodies specific for FHV-1 - for detection, treatment and prevention of FHV-1 infection.

Disclosure; Page 17-18; 53pp; Japanese.

The inventors claim a monoclonal antibody against feline herpes virus (FHV-1). They also claim a recombinant antibody against FHV-1 and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are used in the detection, treatment and prevention of FHV-1. The sequences of the CDRs in the VH of the recombinant anti-FHV-1 antibody are given in AAR54092. The sequences of the CDRs in the VL of the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR sequences are claimed.

Sequence 429 BP; 84 A; 116 C; 109 G; 120 T; 0 other;

Query Match 72.1%; Score 261.8; DB 15; Length 429;

Best Local Similarity 92.6%; Pred. No. 1.3e-70; Mismatches 22; Indels 0; Gaps 0;

Matches 275; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCTCAGTCTG 60

Db 58 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCTCAGTCTG 117

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Db 118 ACTTGTCTTCTCTCTGGGTTTCACTGACACTTCTGTATGGGTGTGAGCTGATTCGT 177

QY 121 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCACACATTACTGGGATGATGACAGCCG 180

Db 178 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCACACATTGTTGGGATGATGTCAGCCG 237

QY 181 TATACCATCCCTGGAAGACCGGCTTACAAATCCCAAGGATACCTCCAGCAACAGGTA 240

Db 238 TATACCATCCCTGGAAGACCGGCTTACAAATCCCAAGGATACCTCCAGCAACAGGTA 297

QY 241 TTCCTCAAGATCACAGTGTGACACTCGAGATACCTCCAGCAATACCTGTGCTGCA 297

Db 298 TTCCTCAAGATCCGACGCTGGACACTGACAGATACCTCCAGCAATACCTGTGCTGCA 354

Search completed: July 11, 2003, 15:23:58

Job time : 243 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 22:13:44 ; Search time 1856 Seconds

(without alignments)
5691.982 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

arched: 2054640 seqs, 14551402878 residues

total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_htg: 3: gb_in: 4: gb_com: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_dr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_ph: 24: em_pl: 25: em_ro: 26: em_sts: 27: em_un: 28: em_vl: 29: em_vl: 30: em_htg_hum: 31: em_htg_in: 32: em_htg_other: 33: em_htg_mus: 34: em_htg_pln: 35: em_htg_rtd: 36: em_htg_mam: 37: em_htg_vrt: 38: em_sy: 39: em_higo_hum: 40: em_higo_mus: 41: em_higo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	316.6	87.2	360	10	MMHCVR3
2	314.6	86.7	420	10	AY090903
3	311.8	85.9	426	6	AX458152
4	305.4	84.1	360	10	MMU22977
5	305.4	84.1	360	10	MMU22979
6	305.4	84.1	360	10	MMU22994
7	303.8	83.7	360	10	MMU22992
8	303.6	83.6	366	6	E07584
9	300.6	82.8	360	10	MMU22981
10	300.6	82.8	360	10	MMU23010
11	300.6	82.8	360	10	MMU23013
12	300.6	82.5	361	10	MMU23004
13	299.6	82.5	360	10	MMU22999
14	299.2	82.4	738	6	E07990
15	299.2	82.4	738	6	I45910
16	298.6	81.5	358	10	MMU23002
17	295.8	81.5	360	10	MMU22983
18	295.8	81.5	360	10	MMU22984
19	295.8	81.5	360	10	MMU23005
20	295.8	81.5	360	10	MMU23009
21	294.4	81.1	360	10	MMU22997
22	294.2	81.0	366	10	MMU22997
23	293.8	80.9	358	10	MMU23000
24	293.4	80.8	359	10	MMU23007
25	293.2	80.8	438	10	S75897
26	291.4	80.3	365	10	MMU22929
27	291.4	80.2	418	6	AR026944
28	290.4	80.0	348	10	MMHCVR4
29	289.8	79.8	365	10	MMU22905
30	289.8	79.8	365	10	MMU22909
31	289.8	79.8	365	10	MMU22911
32	289.8	79.8	365	10	MMU22926
33	289.8	79.8	365	10	MMU22956
34	289.8	79.8	365	10	MMU22957
35	289.8	79.8	20065	2	AC073939
36	289.6	79.8	360	10	MMU22988
37	289.2	79.7	326	10	MMU22986
38	288.4	79.4	363	10	S82427
39	288.2	79.4	365	10	MMU22955
40	287.8	79.3	1410	10	MMU421677
41	285.6	78.7	357	10	S63186
42	285	78.5	318	10	MMU22990
43	285	78.5	330	10	MMU22975
44	282.8	77.9	353	10	MMU22995
45	281.8	77.6	365	10	MMU22907

ALIGNMENTS

RESULT 1	MMHCVR3	360 bp	MRNA	linear	ROD 23-FEB-1994
LOCUS	MMHCVR3				
DEFINITION	M.musculus (A.SW)	MRNA for ASMB1 antibody heavy chain variable			
ACCESSION	X75097.1	GI:414165			
VERSION	X75097.1	GI:414165			
KEYWORDS	antibody; variable region; VH region.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 360)				
TITLE	Monestier, M.				
	Direct Submission				

Pred. No. is the number of results predicted by chance to have a

JOURNAL Submitted (09-SEP-1993) M. Monestier, Center for Molecular Medicine and Immunology, One Bruce Street, Newark, NJ 07103-2763, USA

REFERENCE 2 (bases 1 to 360)

AUTHORS Monestier, M., Losman, M.J., Novick, K.E. and Aris, J.P.

TITLE Molecular analysis of mercury-induced antinuclear antibodies in H-2S mice

JOURNAL J. Immunol. 152 (2), 667-675 (1994)

MEDLINE 94110621

PUBMED 8283044

FEATURES

source

1.360

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/chromosome="12"

/cell_line="ASMB1 hybridoma"

/cell_type="hybridoma"

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/product="ASMB1 heavy chain variable region"

/protein_id="CA52988.1"

/db_xref="GI:414166"

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BASE COUNT 82 a 95 c 89 g 94 t

ORIGIN

Query Match 87.2%; Score 316.6; DB 10; Length 360;

Best Local Similarity 93.9%; Pred. No. 1.1e-91;

Matches 341; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAAGTCTGGCCCTGGGATTTGCAAGCCCTCCAGACCTTCAGTCTG 60

DB 1 CAGGTACTCTGAAAGTCTGGCCCTGGGATTTGCAAGCCCTCCAGACCTTCAGTCTG 60

OY 61 ACTTGTCTTCTCTGGGTTTTCACGAGACCTTGGTATGGGTGGAGCTGGATTCGA 120

DB 61 ACTTGTCTTCTCTGGGTTTTCACGAGACCTTGGTATGGGTGGAGCTGGATTCG 120

OY 121 CAGCCTTCAGGAAGGCTGTGAGTGTGCGACACATTACTGGATGATGACAAAGCCG 180

DB 121 CAGCCTTCAGGAAGGCTGTGAGTGTGCGACACATTACTGGATGATGACAAAGCCG 180

OY 181 TATTAACCATCCCTGTAAGACCGGCTTACAAATCTCCAAAGATACCTCCAGCAACGAT 240

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OY 301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGGAACCTCAGTACCGTCTCC 360

DB 301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGGAACCTCAGTACCGTCTCC 360

OY 298 GTTGATGGTTACTACAGATGCTATGACTACTGGGGTCAAGAACTCAGTACCGTCTCC 357

DB 358 TCA 360

RESULT 2

LOCUS AY090903 420 bp mRNA linear ROD 17-APR-2002

DEFINITION Mus musculus clone GN-2-M4 monoclonal

anti-alpha-1,3-galactosyltransferase IgM heavy chain mRNA, partial

cds.

ACCESSION AY090903

VERSION AY090903.1 GI:20177160

KEYWORDS Mus musculus.

SOURCE Mus musculus.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 420)

AUTHORS Xu, H., Sharma, A., Chen, L., Harrison, C., Wei, Y., Chong, A.S., Logan, J.S., Byrne, G.W. and Shama, A.

TITLE The structure of anti-Gal immunoglobulin genes in naive and stimulated Gal knockout mice

JOURNAL Transplantation 72 (11), 1817-1825 (2001)

MEDLINE 21605873

PUBMED 11740394

REFERENCE 2 (bases 1 to 420)

AUTHORS Xu, H., Sharma, A., Chen, L., Harrison, C., Logan, J.S. and Byrne, G.W.

TITLE Direct Substitution

JOURNAL Submitted (21-MAR-2002) Immunology, Nexttran Inc., 303B College Road East, Plainsboro, NJ 08540, USA

FEATURES

source

1.420

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/db_xref="taxon:10090"

/clone="GN-2-M4"

/cell_type="hybridoma"

/note="generated in alpha-1,3-galactosyltransferase knockout mice"

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BASE COUNT 97 a 123 c 98 g 102 t

ORIGIN

Query Match 86.7%; Score 314.6; DB 10; Length 420;

Best Local Similarity 94.2%; Pred. No. 4.9e-91;

Matches 342; Conservative 0; Mismatches 9; Indels 12; Gaps 1;

QY 1 CAGGTACTCTGAAAGTCTGGCCCTGGGATTTGCAAGCCCTCCAGACCTTCAGTCTG 60

DB 1 CAGGTACTCTGAAAGTCTGGCCCTGGGATTTGCAAGCCCTCCAGACCTTCAGTCTG 60

OY 61 ACTTGTCTTCTCTGGGTTTTCACGAGACCTTGGTATGGGTGGAGCTGGATTCGA 120

DB 61 ACTTGTCTTCTCTGGGTTTTCACGAGACCTTGGTATGGGTGGAGCTGGATTCG 120

OY 121 CAGCCTTCAGGAAGGCTGTGAGTGTGCGACACATTACTGGATGATGACAAAGCCG 180

DB 121 CAGCCTTCAGGAAGGCTGTGAGTGTGCGACACATTACTGGATGATGACAAAGCCG 180

OY 181 TATTAACCATCCCTGTAAGACCGGCTTACAAATCTCCAAAGATACCTCCAGCAACGAT 240

DB 181 TATTAACCATCCCTGTAAGACCGGCTTACAAATCTCCAAAGATACCTCCAGCAACGAT 240

OY 241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGCAATCTACTGTCTCGAAG 300

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OY 301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGGAACCTCAGTACCGTCTCC 360

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DB 349 TCA 351

RESULT 3
LOCUS AX458152 426 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 15 from Patent WO0246237.
ACCESSION AX458152
VERSION AX458152.1 GI:21724902
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Basl, G., Saldanha, J. and Vednock, T.
Humanized antibodies that recognize beta amyloid peptide
Patent: WO 0246237-A 15 13-JUN-2002;
Neuralab Limited (BM) ; Wyeth (US)
FEATURES
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/organism="Mus musculus"
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sig_peptide 1..57
BASE COUNT 94 a 119 c 101 g 112 t
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Best Local Similarity 92.4%; Pred. No. 4e-90;
Matches 341; Conservative 0; Mismatches 22; Indels 6; Gaps 1;
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DB 301 GTC-----TCTCTACGCGCTATGCTATGACATCTGGGGTCAAGAACTCAGTCAC 354
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DB 358 CCCATTACTCCGGTACTAGTCGATGCTATGACACTGCGGTCAAGAACTCAGTCAC 417
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DB 355 GTCCTCCTCA 363
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DB 418 GTCCTCCTCA 426
RESULT 4
LOCUS MMU22977 360 bp mRNA linear ROD 09-APR-1996
DEFINITION Mus musculus Cbl7 SCID immunoglobulin heavy chain V region mRNA,
clone 45-11h, partial cds.
ACCESSION U22977
VERSION U22977.1 GI:780556
KEYWORDS

SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 360)
AUTHORS Young, D. and Kearney, J. F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE
2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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BASE COUNT 84 a 97 c 87 g 92 t
ORIGIN
Query Match 84.1%; Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0%; Pred. No. 4.8e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
DB 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGCTG 60
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DB 361 TCA 363
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DB 358 TCA 360
RESULT 5
LOCUS MMU22979 360 bp mRNA linear ROD 09-APR-1996
LOCUS

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-12h, partial cds.

ACCESSION U22979
VERSION U22979.1 GI:780560

KEYWORDS Mus musculus.

SOURCE Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
TITLE Ig+ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

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CDS
BASE COUNT 84 a 98 c 87 g 91 t
ORIGIN

Query Match 84.1%; Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0%; Pred. No. 4.8e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGATATTGAGCCCTCCAGACCTCAGTCTG 60
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QY 361 TCA 363
361 TCA 363
Db 358 TCA 360

RESULT 6
LOCUS MMU22994
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.

ACCESSION U22994
VERSION U22994.1 GI:780590

KEYWORDS Mus musculus.

SOURCE Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
TITLE Ig+ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

FEATURES
SOURCE location/Qualifiers
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/strain="CB17 SCID"
/sub_species="domesticus"
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CDS
BASE COUNT 84 a 95 c 87 g 94 t
ORIGIN

Query Match 84.1%; Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0%; Pred. No. 4.8e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGATATTGAGCCCTCCAGACCTCAGTCTG 60
1 CAGGTACTCTGAAGAAGTCTGGCCCTGGATATTGAGCCCTCCAGACCTCAGTCTG 60
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QY 361 TCA 363
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RESULT 7
MWU22992 360 bp mRNA linear ROD 09-APR-1996
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-26h, partial cds.
ACCESSION U22992
VERSION U22992.1 GI:780586
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D. and Kearney, J. F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PubMed 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

FEATURES
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CDS
83 a 99 c 87 g 91 t

BASE COUNT 83 a 99 c 87 g 91 t

ORIGIN
Query Match 83.7%; Score 303.8; DB 10; Length 360;
Best Local Similarity 91.7%; Pred. No. 1.6e-87;
Matches 333; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 CAGGTTACTGGAAGAGTCTGGCCCTGGATATGACGCCCTCCAGACCTCAGTCTG 60
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QY 61 ACTGTCTCTCTCTGGGTTTCACTGAGCACTCTGCTATGAGGTGAGCTGATTGCA 120
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QY 121 CAGCCTTCAGGAAGAGGTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCGC 180
DB 121 CAGCCTTCAGGAAGAGGTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCGC 180
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QY 241 TTCTCAAGATCACACAGTGTGAGACCTGAGATACCTGCAATACCTACTGTGTCGAAG 300

DB 241 TTCTCAAGATCACACAGTGTGAGACCTGAGATACCTGCAATACCTACTGTGTCGAAG 300
QY 301 GTCTCTTACTGCTTATGATGACTGAGTGGGTCAAGACCTCAGTACCGCTCTCC 360
DB 301 G---CTAGTAGTAGTACTTACTGACTGAGGCGCAAGCACCCTTACAGTCTCC 357
QY 361 TCA 363
DB 358 TCA 360

RESULT 8
E07584 366 bp RNA linear PAT 29-SEP-1997
LOCUS E07584
DEFINITION Gene fragment coding the variable region in the heavy chain.
ACCESSION E07584
VERSION E07584.1 GI:2175719
KEYWORDS JP 1994141885-A/L.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 366)
AUTHORS Eda, Y., Nagatomi, K., Shiosaki, K., Maeda, H., Kurumi, K. and
Tokiyoshi, Y.
TITLE MONOCLONAL ANTIBODY
JOURNAL Patent: JP 1994141885-A 1 24-MAY-1994;
OS Chemo SERO THERAPEUT RES INST
PN JP 1994141885-A/1
PD 24-MAY-1994
PF 05-NOV-1992 JP 1992322476
PI ED A YASUYUKI, NAGATOMI KIYOSHI, SHIOSAKI KOICHI, PI MAEDA
HIROAKI,
PI KURUMI KAZUHIKO, TOKIYOSHI YUKIO
PC C12P21/08.C07K15/28//C12N15/06.C12N15/13.C12N15/62.G01N33/569,
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CC topology: linear;
FH key Location/Qualifiers
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1..366
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BASE COUNT 85 a 98 c 84 g 99 t

ORIGIN
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Best Local Similarity 91.3%; Pred. No. 1.8e-87;
Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

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DB 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGAAACAGGTA 240
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QY	301	G---TCTCTTACTGCTACTGCTATGAGACTACTGGGTCGAAGAACTCAGTACCCTC	357
Db	301	GTCTTCTTAGTAACTCCGATTTTATGACACCACTGGGTCGAAGAACTCAGTACCCTC	360
QY	358	TTCTCA	363
Db	361	TTCTCA	366

RESULT 9	
MMU22981	
LOCUS	360 bp mRNA linear ROD 09-APR-1996
DEFINITION	Mmus musculus Cbl7 SCID immunoglobulin heavy chain V region mRNA,
	c1one 45-13n, partial cds.
ACCESSION	U22981
VERSION	U22981.1 GI:780564

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 360) Young, D. and Kearney, J.F.
TITLE	Sequence analysis and antigen binding characteristics of Ig SCID Ig+ mice
JOURNAL	Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE	96053543
PUBMED	7547707
REFERENCE	2 (bases 1 to 360)
AUTHORS	Young, D.C.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

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		/tissue_type="spleen"
		<1..>360
CDS		/codon_start=-1
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		/db_xref="GI:780565"
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BASE COUNT	83 a	99 c
ORIGIN		87 g 91 t

Query Match	82.8%	Score 300.6	DB 10	Length 360
Best Local Similarity	91.2%	Pred. No. 1.7e-86		
Matches	331	Conservative 0	Mismatches 29	Indels 3
			Gaps 1	
QY	1	CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTGTG	60	
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QY	61	ACTTGTCTTCTCTCTGCGGTTTCACTAGACACTTCTGGTATGGGTGTGAGCTGATTGCA	120	
Db	61	ACTGTCTTCTCTCTCTGCGGTTTCACTAGACACTTCTGGTATGGGTGTGAGCTGATTGCT	120	
QY	121	CAGCCTTCAGGAAAGGCTCTGGAATGGCTGGCACACATTACTGGGATGATGACAAAGCC	180	
Db	121	CAGCCTTCAGGAAAGGCTCTGGAATGGCTGACACACATTACTGGGATGATGACAAAGCC	180	

QY	181	TATTAACCCATCCCTGTAAGACCGGGCTTCACATATCTCAAGGTTACTCTCAGACACAGGTA	240
Db	181	TATTAACCCATCCCTGTAAGACCGGGCTTCACATATCTCAAGGTTACTCTCAGACACAGGTA	240
QY	241	TTTCCTCAAGATCAGCAGTGTGGACACTCGAGATACCTGCCATCTACTGTGCTCGAAGG	300
Db	241	TTTCCTCAAGATCAGCAGTGTGGACACTCGAGATACCTGCCATCTACTGTGCTCGAAGG	300
QY	301	GTCTCTCTTAAGTCCCTATGCTATGTGCATCTACGGGGTCAAGGAACTTAGTCACCGTCTCC	360
Db	301	G---CTCTAGGTAGTACCTACTTTGTATCTACGTGGGGCAGGACCACTCTTCACAGTCTCC	357
QY	361	TCA	363
Db	358	TCA	360

RESULT 10	
LOCUS	MMU23010
DEFINITION	MMU23010 360 bp mRNA linear ROD 20-SEP-2001
ACCESSION	Mus musculus Cbl17 SCID immunoglobulin heavy chain V region mRNA,
VERSION	U23010
KEYWORDS	U23010.1 GI:780622
SOURCE	
ORGANISM	Mus musculus.
	Mus musculus.

REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED
1 (bases 1 to 360) Young, D. and Kearney, J. F. Sequence analysis and antigen binding characteristics of Ig SCID 1g+ mice	Int. Immunol. 7 (5), 807-819 (1995) 96053543
2 (bases 1 to 360) Young, D. C. Direct Submussion Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA	7547707

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BASE COUNT		83 a 99 c 87 g 91 t
ORIGIN		

Query Match	82.8%;	Score 300.6;	DB 10;	Length 360;
Best Local Similarity	91.2%;	Pred. No. 1.7e-86;		
Matches 331;	Conservative 0;	Mismatches 29;	Indels 3;	Gaps 1;
QY	1	CAGGTTACTCTGGAAGAAGTCTGGCCCTTGGATATTGCAGGCCCTCCAGACCTCTAGTCTG	60	
Db	1	CAGGTTACTCTGGAAGAAGTCTGGCCCTTGGATATTGCAGGCCCTCCAGACCTCTAGTCTG	60	
QY	61	ACTGTTCTTCTCTCTGGGTTTTCACATGACACTCTCGTATGGGCTGAGCTGGATTCGA	120	
Db	61	ACTGTTCTTCTCTCTGGGTTTTCACATGACACTCTCGTATGGGCTGAGCTGGATTCGT	120	

QY 121 CAGCTTCAGGAAGGGCTGAGAGTGGCTGGACACATTCTATGCGATGATGACAGGCG 180
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QY 241 TTCCTCAAGATCACCAGTGTGACACTGCAATATCTGCCATATCTACTGTGCTGGAAG 300
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DB 241 TTCCTCAAGATCACCAGTGTGACACTGCAATATCTGCCATATCTACTGTGCTGGAAG 300
QY 301 GTCCTCTAAGTACCTATGCTATGAGTACTGAGGAGTCAAGAACCTGATACCGTCTCC 360
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DB 301 G---CTTAGGTAGTACTACTTGTGACTTACTGAGGAGGCGCAGGACACACTCTCAGAGTCTCC 357
QY 361 TCA 363
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DB 358 TCA 360

RESULT 11
MMU23013 360 bp mRNA linear ROD 20-SEP-2001
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-8h, partial cds.
ACCESSION U23013
VERSION U23013.1 GI:780628
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young,D.C.
TITLE Direct Submision
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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BASE COUNT 83 a 99 c 87 g 91 t
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Query Match 82.8%; Score 300.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred. No. 1.7e-86;
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DB 1 CAGGTTACTCTGAAGAAGTCTGGCCCTGGATATTCAGGCTCCAGACCTCAGTCTG 60
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DB 61 ACTGTTCTTCTCTGTTGGTTTTCACACTGACACTTCTGTAAGGTTGAGCTGATTCGT 120
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DB 358 TCA 360

RESULT 12
MMU23004 361 bp mRNA linear ROD 20-SEP-2001
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-3h, partial cds.
ACCESSION U23004
VERSION U23004.1 GI:780610
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 361)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 361)
AUTHORS Young,D.C.
TITLE Direct Submision
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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BASE COUNT 83 a 99 c 88 g 91 t
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Query Match 82.8%; Score 300.6; DB 10; Length 361;

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	topology:	Linear;	
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source		/db_xref='taxon:32644'	

BASE COUNT 187 a 189 c 180 g 182 t
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QY 1 CAGGTTACTCTGAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
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QY 61 ACTGTTCTTCTCTGCGTTTTCACAGCACTTCTGATGAGGTGAGCTGATTCGA 120
DB 427 ACTGTTCTTCTCTGCGTTTTCACAGCACTTCTGATGAGGTGAGCTGATTCGT 486
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DB 181 TATAACCCATCCCTGAAGAGCGCGCTTACATCTCCAGATACCTCCAGCAACAGSTA 240
DB 547 TATAACCCATCCCTGAAGAGCGCGCTTACATCTCCAGATACCTCCAGCAACAGSTA 606
QY 241 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGCCACATCTACTGCTCGAAG- 299
DB 607 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGCCACATCTACTGCTCGAAGA 666
QY 300 -----GGTCTCTTACTGCTATGCTATGAGACTAGTGGGTCAGGAACCTCAGTC 351
DB 667 AGTCTCTATGTTAATTTGGGGGAGCTATGCTATGAGACTAGTGGGTCAGGAACCTCAGTC 726
QY 352 ACCGTCCTCTCA 363
DB 727 ACCGTCCTCTCA 738

RESULT 15

LOCUS 145910 738 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5639455.
ACCESSION 145910
VERSION 145910.1 GI:2469875
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 738)
AUTHORS Shimamura,T., Nakazawa,H. and Hamuro,J.
TITLE Immunosuppressant
JOURNAL Patent: US 5639455-A 6 17-JUN-1997;
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BASE COUNT 187 a 189 c 180 g 182 t
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Best Local Similarity 90.1%; Pred. No. 5,1e-86;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 367 CAGGTTACTCTGAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 426
QY 61 ACTGTTCTTCTCTGCGTTTTCACAGCACTTCTGATGAGGTGAGCTGATTCGA 120
DB 427 ACTGTTCTTCTCTGCGTTTTCACAGCACTTCTGATGAGGTGAGCTGATTCGT 486
QY 121 CAGCCTTCAGGAAGAGGCTGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 180
DB 487 CAGCCTTCAGGAAGAGGCTGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAAACAC 546
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DB 607 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGCCACATCTACTGCTCGAAGA 666
QY 300 -----GGTCTCTTACTGCTATGCTATGAGACTAGTGGGTCAGGAACCTCAGTC 351
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QY 352 ACCGTCCTCTCA 363
DB 727 ACCGTCCTCTCA 738

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and is derived by analysis of the total score distribution.

SUMMARIES

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5	299.2	82.4	738	1	US-08-197-834-6
6	296.4	81.7	417	5	PCT-US95-07372-9
7	291	80.2	418	2	US-08-535-501A-28
8	291	80.2	418	3	US-09-205-231-28
9	261.8	72.1	462	1	US-08-436-463-1
10	250.8	69.1	812	1	US-08-408-133-1
11	250.8	69.1	812	1	US-08-454-683-1
12	250.8	69.1	812	2	US-08-116-778E-16
13	250.8	69.1	812	2	US-08-454-680-1
14	250.8	69.1	812	2	US-08-438-562-16
15	250.8	69.1	812	2	US-08-483-528B-16
16	250.8	69.1	812	3	US-08-673-799C-16
17	250.8	69.1	812	4	US-09-393-385B-16
18	250.8	69.1	812	4	US-09-225-332B-1
19	190.6	52.5	423	2	US-08-345-321-9
20	190.2	52.4	613	3	US-08-545-809A-5
21	185.4	51.1	418	2	US-08-553-501A-58
22	185.4	51.1	418	2	US-09-205-231-58
23	185.4	51.1	1607	3	US-09-049-672A-14
24	183.8	50.6	418	2	US-08-553-501A-60
25	183.8	50.6	418	3	US-09-205-231-60
26	181.2	49.9	546	3	US-08-545-809A-26
27	172.6	47.5	630	3	US-08-545-809A-10

28	171	47.1	423	2	US-08-483-636-11	Sequence 11, Appl
29	171	47.1	423	2	US-08-483-632-11	Sequence 11, Appl
30	165	45.5	714	4	US-09-142-974B-2	Sequence 2, Appl
31	165	45.5	1173	4	US-09-142-974B-4	Sequence 4, Appl
32	163.2	45.0	378	1	US-08-488-376-15	Sequence 15, Appl
33	163.2	45.0	378	2	US-08-634-223-15	Sequence 15, Appl
34	163.2	45.0	378	2	US-08-634-224-15	Sequence 15, Appl
35	163.2	45.0	378	2	US-08-634-400-15	Sequence 15, Appl
36	163.2	45.0	378	2	US-08-635-878-15	Sequence 15, Appl
37	163.2	45.0	378	2	US-08-770-057-15	Sequence 15, Appl
38	163.2	45.0	378	4	US-09-335-697B-15	Sequence 15, Appl
39	163.2	45.0	378	4	US-09-335-697B-15	Sequence 15, Appl
40	163.2	45.0	1428	1	US-08-488-376-19	Sequence 19, Appl
41	163.2	45.0	1428	2	US-08-634-223-19	Sequence 19, Appl
42	163.2	45.0	1428	2	US-08-634-224-19	Sequence 19, Appl
43	163.2	45.0	1428	2	US-08-634-400-19	Sequence 19, Appl
44	163.2	45.0	1428	2	US-08-635-878-19	Sequence 19, Appl
45	163.2	45.0	1428	2	US-08-770-057-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-3
Sequence 3, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
US-08-483-636-3

Query Match 86.3%; Score 313.4; DB 2; Length 483;
Best Local Similarity 91.5%; Pred. No. 5.8e-99;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATATGAGCCCTCCAGACCTCAGTCTG 60
DB 121 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATATGAGCCCTCCAGACCTCAGTCTG 180
QY 61 ACTTGTCTTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGGATTGCA 120
DB 181 ACTTGTCTTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGGATTGCT 240
QY 121 CAGCCTTCAGAAAGGCTGTGAGTGGCTGGACACATTTACTGGATGATGACAGCCG 180
DB 241 CAGCCTTCAGAAAGGCTGTGAGTGGCTGGACACATTTACTGGATGATGACAGCCG 300
QY 181 TATTAACCCATCCCTGAAGAGCCGGCTTACATCTCCAAAGATACCTCCAGCAGAGTA 240
DB 301 TATTAACCCATCCCTGAAGAGCCGGCTTACATCTCCAAAGATACCTCCAGCAGAGTA 360
QY 241 TTCCCTCAAGATCAGCACTGTGACACTGAGATACCTCCATCTACTGTGCTGAGAG 300
DB 361 TTCCCTCAAGATCAGCACTGTGACACTGAGATACCTCCATCTACTGTGCTGAGAG 420
QY 301 GTCTCTCTAAGTCCCTATGCTATGAGACTACTGGGGTCAAGAACCTGACCGTCTCC 360
DB 421 GAGACTGTGTTCTACTGTGACTTCGATGTCTGGGGCCAGGAGACACGCTCAGCTCTCC 480
QY 361 TCA 363
DB 481 TCA 483

RESULT 2

US-08-483-632-3
Sequence 3, Application US/08483632
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113666
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
US-08-483-632-3.

Query Match 86.3%; Score 313.4; DB 2; Length 483;
Best Local Similarity 91.5%; Pred. No. 5.8e-99;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATATGAGCCCTCCAGACCTCAGTCTG 60
DB 121 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATATGAGCCCTCCAGACCTCAGTCTG 180
QY 61 ACTTGTCTTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGGATTGCA 120
DB 181 ACTTGTCTTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGGATTGCT 240
QY 121 CAGCCTTCAGAAAGGCTGTGAGTGGCTGGACACATTTACTGGATGATGACAGCCG 180
DB 241 CAGCCTTCAGAAAGGCTGTGAGTGGCTGGACACATTTACTGGATGATGACAGCCG 300
QY 181 TATTAACCCATCCCTGAAGAGCCGGCTTACATCTCCAAAGATACCTCCAGCAGAGTA 240
DB 301 TATTAACCCATCCCTGAAGAGCCGGCTTACATCTCCAAAGATACCTCCAGCAGAGTA 360
QY 241 TTCCCTCAAGATCAGCACTGTGACACTGAGATACCTCCATCTACTGTGCTGAGAG 300
DB 361 TTCCCTCAAGATCAGCACTGTGACACTGAGATACCTCCATCTACTGTGCTGAGAG 420
QY 301 GTCTCTCTAAGTCCCTATGCTATGAGACTACTGGGGTCAAGAACCTGACCGTCTCC 360
DB 421 GAGACTGTGTTCTACTGTGACTTCGATGTCTGGGGCCAGGAGACACGCTCAGCTCTCC 480
QY 361 TCA 363
DB 481 TCA 483

RESULT 3

US-08-483-636-9
Sequence 9, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA

ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
US-08-483-636-9

Query Match 85.9%; Score 311.8; DB 2; Length 423;
Best Local Similarity 91.2%; Pred. No. 1.9e-98;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGTTACTCTGAAAGAGCTGCGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 61 CAGTTACTCTGAAAGAGCTGCGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 120
QY 61 ACTGTTCTTCTCTGCGGTTTTCACCTGACCACTTCTGATGGGTGAGCTGATTCGA 120
DB 121 ACTGTTCTTCTCTGCGGTTTTCACCTGACCACTTCTGATGGGTGAGCTGATTCGT 180
QY 121 CAGCTTCAGGAAGAGGCTGAGAGGCTGGACACATTTACTGGATGATGACAAGCGC 180
DB 181 CAGCTTCAGGAAGAGGCTGAGAGGCTGGACACATTTACTGGATGATGACAAGCGC 240
QY 181 TATAACCCATCCCTGAAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
DB 241 TATAACCCATCCCTGAAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 300
QY 241 TTCTCTCAAGATCACCAGTGTGAGACACTGAGATACGTCACATACCTACTGTGCTGAAGG 300
DB 301 TTCTCTCAAGATCACCAGTGTGAGACACTGAGATACGTCACATACCTACTGTGCTGAAGG 360
QY 301 GTCTCTCAACTGCGCTATGATGACATCTGAGGCTCAAGAACCTCAGTCCGTCCTCC 360
DB 361 GAGACTGTGTTCTACTGTAATCTGATGATCTGAGGCGCAGGAGACCGTCAACGCTCTCC 420
QY 361 TCA 363
DB 421 TCA 423

RESULT 4
US-08-483-632-9

Sequence 9, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
US-08-483-632-9

Query Match 85.9%; Score 311.8; DB 2; Length 423;
Best Local Similarity 91.2%; Pred. No. 1.9e-98;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGTTACTCTGAAAGAGCTGCGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 61 CAGTTACTCTGAAAGAGCTGCGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 120
QY 61 ACTGTTCTTCTCTGCGGTTTTCACCTGACCACTTCTGATGGGTGAGCTGATTCGA 120
DB 121 ACTGTTCTTCTCTGCGGTTTTCACCTGACCACTTCTGATGGGTGAGCTGATTCGT 180
QY 121 CAGCTTCAGGAAGAGGCTGAGAGGCTGGACACATTTACTGGATGATGACAAGCGC 180
DB 181 CAGCTTCAGGAAGAGGCTGAGAGGCTGGACACATTTACTGGATGATGACAAGCGC 240
QY 181 TATAACCCATCCCTGAAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
DB 241 TATAACCCATCCCTGAAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 300

OY 1 CAGGTTACTCTGAAAGAGCTGTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
 ||||| - - - - -
 Db 367 CAGGTTAACTCGAGAGAGCTGTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 428

OTHER INFORMATION: nucleotides 1 through 57. "

FEATURE:
NAME/KEY: misc_feature
LOCATION: 58..417
OTHER INFORMATION: /note- "Mature peptide encoded by
OTHER INFORMATION: nucleotides 58 through 417."
PCT-US95-07372-9

Query Match 81.7%; Score 296.4; DB 5; Length 417;
Best Local Similarity 90.6%; Pred. No. 4.1e-93;
Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1 CAGGTTACTGGAAGAGTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTGAGTCTG 60
DB 58 CAGGTTACTGGAAGAGTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTGAGTCTG 117
QY 61 ACTGTTCTTCTGCTGGGTTTCTGACGACCTCTGTAAGGCTGAGCTGATGCA 120
DB 118 ACTGTTCTTCTGCTGGGTTTCTGACGACCTCTGTAAGGCTGAGCTGATGCA 177
QY 121 CAGCCTTCAGGAAGAGGCTGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 180
DB 178 CAGCCTTCAGGAAGAGGCTGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 237
QY 181 TATAACCCAGTCCCTGAAGAGCGGCTTACAAATCTCAAGATACCTCCAGACAGGTA 240
DB 238 TATAACCCAGTCCCTGAAGAGCGGCTTACAAATCTCAAGATACCTCCAGACAGGTA 297
QY 241 TTCTCAAGATCAGCAGTGTGACACATGAGATCTGCGCATCTACTGCTGCGAAG 300
DB 298 TTCTCAAGATCAGCAGTGTGACACATGAGATCTGCGCATCTACTGCTGCGAAG 357
QY 301 GTCTCTTAAGTGGCTTATGATGACTGAGGCTCAAGAACCTCAGTACCGCTCC 360
DB 358 ATGAT---GATTACGACGCTATGACTACTGGGGTCAAGAACCTCAGTACCGCTCC 414
QY 361 TC 362
DB 415 TC 416

RESULT 7
US-08-553-501A-28
Sequence 28, Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..417
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..417
US-08-553-501A-28

Query Match 80.2%; Score 291; DB 2; Length 418;
Best Local Similarity 89.5%; Pred. No. 3.1e-91;
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTTACTGGAAGAGTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTGAGTCTG 60
DB 58 CAGGTTACTGGAAGAGTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTGAGTCTG 117
QY 61 ACTGTTCTTCTGCTGGGTTTCTGACGACCTCTGTAAGGCTGAGCTGATGCA 120
DB 118 ACTGTTCTTCTGCTGGGTTTCTGACGACCTCTGTAAGGCTGAGCTGATGCA 177
QY 121 CAGCCTTCAGGAAGAGGCTGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 180
DB 178 CAGCCTTCAGGAAGAGGCTGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 237
QY 181 TATAACCCAGTCCCTGAAGAGCGGCTTACAAATCTCAAGATACCTCCAGACAGGTA 240
DB 238 TATAACCCAGTCCCTGAAGAGCGGCTTACAAATCTCAAGATACCTCCAGACAGGTA 297
QY 241 TTCTCAAGATCAGCAGTGTGACACATGAGATCTGCGCATCTACTGCTGCGAAG 300
DB 298 TTCTCAAGATCAGCAGTGTGACACATGAGATCTGCGCATCTACTGCTGCGAAG 357
QY 301 GTCTCTTAAGTGGCTTATGATGACTGAGGCTCAAGAACCTCAGTACCGCTCC 360
DB 358 GAGAT---TACGACGAAGTATGACTACTGGGGTCAAGAACCTCAGTACCGCTCC 414
QY 361 TCA 363
DB 415 TCA 417

RESULT 8
US-09-205-231-28
Sequence 28, Application US/09205231
Patent No. 6121423
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..417
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..417
US-09-205-231-28

Query Match 80.2%; Score 291; DB 3; Length 418;
Best Local Similarity 89.5%; Pred. No. 3,1e-91;
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 60
58 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 117
61 ACTTGTCTTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGAGTTGCA 120
118 ACTTGTCTTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGAGTTGCT 177
121 CAGCCTTCAGAAAGAGTCTGGAGTGGCTGGCAGACATTTACTGGGATGAGCAAGCGC 180
178 CAGCCTTCAGAAAGAGTCTGGAGTGGCTGGCAGACATTTGGTGAATGATTAATAC 237
181 TATAACCATCCCTGAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 240
238 TATAACCATCCCTGAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 297
241 TTCTCTCAAGATCAGCACTGAGACCTCGAGATACCTCCAGCAATCTGCTCGAAG 300
298 TTCTCTCAAGATCAGCACTGAGACCTCGAGATACCTCCAGCAATCTGCTCGAATG 357
301 GTCTCTCAAGATCAGCACTGAGACCTCGAGATACCTCCAGCAATCTGCTCGAATG 360
358 GAGAT---TACGACGAAGCTATGAGACTACTGGGGTCAAGAAACCTGACCGTCC 414
361 TCA 363
415 TCA 417

RESULT 9

US-08-436-463-1
Sequence 1, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTI-BODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 21..449
US-08-436-463-1

Query Match 72.1%; Score 261.8; DB 1; Length 462;
Best Local Similarity 92.6%; Pred. No. 4,2e-81;
Matches 275; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 60
78 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 137
61 ACTTGTCTTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGAGTTGCA 120
138 ACTTGTCTTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGAGTTGCT 197
121 CAGCCTTCAGAAAGAGTCTGGAGTGGCTGGCAGACATTTACTGGGATGAGCAAGCGC 180
198 CAGCCTTCAGAAAGAGTCTGGAGTGGCTGGCAGACATTTGGTGAATGATTAATAC 257
181 TATAACCATCCCTGAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 240
258 TATAACCATCCCTGAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 317
241 TTCTCTCAAGATCAGCACTGAGACCTCGAGATACCTCCAGCAATCTGCTCGA 297
318 TTCTCTCAAGATCAGCACTGAGACCTCGAGATACCTCCAGCAATCTGCTCGA 374

RESULT 10
US-08-408-133-1
Sequence 1, Application US/08408133
Patent No. 5750078
GENERAL INFORMATION:
APPLICANT: SHITARA, Kenya
APPLICANT: HANAI, No. 5750078uo
APPLICANT: HASEGAWA, Mamoru
APPLICANT: MIYAJI, Hitomasa
APPLICANT: KUMAWA, Yoshihisa
TITLE OF INVENTION: Process for Producing Humanized Chimera
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: No. 5750078th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,133
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (803)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: Hybridoma KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
OTHER INFORMATION: /product- "RAT IMMUNOGLOBULIN HEAVY"
OTHER INFORMATION: CHAIN VARIABLE REGION"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 429..806)
OTHER INFORMATION:
US-08-408-133-1
Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGTATGGGTGTGAGCTGGATTGCA 120
DB 501 ACTTGCTCTTCTCTGGGTTTTCACGTGACACTTATGATGTATGTGTGGGTGATTCGT 560
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCC 180
DB 561 CAGTCTTCAGGAGGAGGCTGTGAGTGGCTGCAACCGTTTGCTGAGATGCTAAAGTAC 620
QY 181 TATAACCAACCCGAGAGAGCGGCTTACATCTCCAAAGTACTCTCAGAACCGTA 240
DB 621 TACATTCATCTGTGAATAAACCGGCTCAATCTCCAAAGACACTCCAAACCAAGCA 680
QY 241 TTCCTCAAGATCACAGTGTGACACATCGAGATCTGACATCTACTGTCTCAAGG 300
DB 681 TTCCTCAAGATCACAGTGTGACACATCGAGATCTGACATCTACTGTCTGAGGAGA 740
QY 301 GTCTCTTACTGCTTATGCTA---TGCATCTAGGGGTCAAGAACCTCAGTACCGTC 357
DB 741 GGGGCTACGAGGGTATATGATGAGCTTGTGATTACTGGGGCCACGAGTCATGTCACAGTC 800
QY 358 TTCCTCA 363
DB 801 TTCCTCA 806
RESULT 11
US-08-454-683-1
Sequence 1, Application US/08454683
Patent No. 5807548
GENERAL INFORMATION:
APPLICANT: SHITARA, Kenya
APPLICANT: HANAI, No. 5807548uo
APPLICANT: HASEGAWA, Mamoru
APPLICANT: MIYAJI, Hitomasa
APPLICANT: KUMAWA, Yoshihisa
TITLE OF INVENTION: Process for Producing Humanized Chimera
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: No. 5807548th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,683
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/408,133
FILING DATE:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (803)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE: N
STRAIN: Hybridoma KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
OTHER INFORMATION: /product="RAT IMMUNOGLOBULIN HEAVY
OTHER INFORMATION: CHAIN VARIABLE REGION"
FEATURE:
NAME/KEY: s1g_peptide
LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 429..806)
OTHER INFORMATION:
US-08-454-683-1

Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTGTGAAGAGCTGGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 60
DB 441 CAGGTTACTGTGAAGAGATCTGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTCTGGGTTTTCAGTGCACCTTGTGTGGTGTGAGCTGGATTGCA 120
DB 501 ACTTGCTCTTCTCTCTGGGTTTTCAGTGCACCTTGTGTGGTGTGAGCTGGATTGCGT 560
QY 121 CAGCCTTCAGGAAGGCTGTGGAGTGGCTGGCAGACATTTCAGTGGATGTGACAAAGCC 180
DB 561 CAGCTTCAGGAAGGCTGTGGAGTGGCTGGCAGAACTTTGTGGAGTGTGCTAAAGTAC 620
QY 181 TATAACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGATACCTCCAGACCAAGCA 240
DB 621 TACAATCCATCTCTGAAAAACCGCTCACAATCTCCAGAGACACCTCCAAACCAAGCA 680
QY 241 TTCCCTCAAGATCACCAAGTGTGACACTCGAGATACCTGCAATACCTACTGCTCGAAG 300
DB 681 TTCCCTCAAGATCACCAATATGAGACACTGACAGATACCTGCAATATCTACTGCTGGGAGA 740
QY 301 GTCTCTACTACCTGCTATGCTA---TGAGTACTGGGGTCAAGAACCTGAGTCAAGCCTG 357
DB 741 GGGGCTACGAGAGGATATAGTACCTTTGATTACTGGGGCCACGAGATCATGTACAGTTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 12
US-08-116-778E-16
Sequence 16, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUNANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 261..267
US-08-116-778E-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTGTGAAGAGCTGGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 60
DB 441 CAGGTTACTGTGAAGAGATCTGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTCTGGGTTTTCAGTGCACCTTGTGTGGTGTGAGCTGGATTGCA 120
DB 501 ACTTGCTCTTCTCTCTGGGTTTTCAGTGCACCTTGTGTGGTGTGAGCTGGATTGCGT 560
QY 121 CAGCCTTCAGGAAGGCTGTGGAGTGGCTGGCAGACATTTCAGTGGATGTGACAAAGCC 180
DB 561 CAGCTTCAGGAAGGCTGTGGAGTGGCTGGCAGAACTTTGTGGAGTGTGCTAAAGTAC 620
QY 181 TATAACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGATACCTCCAGACCAAGCA 240
DB 621 TACAATCCATCTCTGAAAAACCGCTCACAATCTCCAGAGACACCTCCAAACCAAGCA 680
QY 241 TTCCCTCAAGATCACCAAGTGTGACACTCGAGATACCTGCAATACCTACTGCTCGAAG 300
DB 681 TTCCCTCAAGATCACCAATATGAGACACTGACAGATACCTGCAATATCTACTGCTGGGAGA 740
QY 301 GTCTCTACTACCTGCTATGCTA---TGAGTACTGGGGTCAAGAACCTGAGTCAAGCCTG 357
DB 741 GGGGCTACGAGAGGATATAGTACCTTTGATTACTGGGGCCACGAGATCATGTACAGTTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 13
US-08-454-680-1

Sequence 1, Application US/08454680
Patent No. 5866692
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA
TITLE OF INVENTION: ANTIBODY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,680
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/408,133
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE: 17-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-238375
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 249-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 300..440
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 430..806)
US-08-454-680-1
Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
1 CAGGTTACTGTGAAGAATCTGGCCCTGGGATATGCAAGCCCTCCAGACCTCAGCTG 60
|||||

DB 441 CAGGTTACTGTGAAGAATCTGGCCCTGGGATATGCAAGCCCTCCAGACCTCAGCTG 500
QY 61 ACTGTTCTTCTCTCTGGGTTTTCAGTGACCACTTCTGATGAGGTGAGTGCATTCGA 120
|||||
DB 501 ACTTGCTCTTCTCTGCTGACGACACTTGTGATGTGTGGCTGGATTCTG 560
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGACACATTTACTGGGATGATGACACCGC 180
|||||
DB 561 CAGCTTCAGGGAAGGGTCTGGAGTGGCTGGACAACTTTGGTGGAGTGTACTAC 620
QY 181 TATAACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATACCTCAGCAACAGCA 240
|||||
DB 621 TACAAATCCATCTCTGAAAAACCGCTCAATCTCCAAAGACACCTCAACAAACAGCA 680
QY 241 TTCCTCAATGATCAGAGTGTGGACATGACATGATGATGATGATGATGATGATGATG 300
|||||
DB 681 TTCCTCAATGATCAGAGTGTGGACATGACATGATGATGATGATGATGATGATGATG 740
QY 301 GTCTCTTAATGCTTATGCTA--TGAGTACTGGGGTCAAGAACCTGATCAGCTC 357
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DB 741 GGGGCTACGAGGAGGTATGATGAGCTTGTATGATGAGGGCCAGAGTATGATGATGATG 800
QY 358 TCCTCA 363
|||||
DB 801 TCCTCA 806

RESULT 14
US-08-438-562-16
Sequence 16, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

Tue Jul 15 10:45:08 2003

us-09-759-112a-5.ini

Page

MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: HYBRIDOMA KM50
STRAIN: HYBRIDOMA KM50
FEATURE: TATA_signal
NAME/KEY: TATA_signal
LOCATION: 261..267
US-08-438-562-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTCAGACCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTCAGACCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTGTTCTTCTCTCTGGGTTTTCACCTGAGCATTCTGTGTATGGGTGTGAGCTGATTCGA 120
DB 501 ACTGTTCTTCTCTCTGGGTTTTCACCTGAGCATTCTGTGTATGGGTGTGAGCTGATTCGT 560
QY 121 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCACAATTACTGGGATGATGACAAAGCC 180
DB 561 CAGTCTTCAGGAGGCTCTGAGTGGCTGGCACAATTACTGGGATGATGACAAAGCC 620
QY 181 TATTAACCATCCCTGAAAGAGCCGCTTACAAATCTCCAGAGATACCTCCAGAACAGGTA 240
DB 621 TACAAATCCATCTGAAAGAGCCGCTTACAAATCTCCAGAGATACCTCCAGAACAGGTA 680
QY 241 TTCTCTAAGATCACCAGTGTGACACTCGAGATACCTGCAATCTGCTGCTGGAAG 300
DB 681 TTCTCTAAGATCACCAGTGTGACACTCGAGATACCTGCAATCTGCTGCTGGAAG 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTGAAGAACCTCAGTCAAGCTC 357
DB 741 GGGGCTACGAGGATATAGTGTGAGCTTGTATTACTGGGGCCACGAGATCATGTGCACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 15
US-08-483-528B-16
Sequence 16, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUNAKI, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: HYBRIDOMA KM50
STRAIN: HYBRIDOMA KM50
FEATURE: TATA_signal
NAME/KEY: TATA_signal
LOCATION: 261..267
US-08-483-528B-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTCAGACCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTCAGACCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTGTTCTTCTCTCTGGGTTTTCACCTGAGCATTCTGTGTATGGGTGTGAGCTGATTCGA 120
DB 501 ACTGTTCTTCTCTCTGGGTTTTCACCTGAGCATTCTGTGTATGGGTGTGAGCTGATTCGT 560
QY 121 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCACAATTACTGGGATGATGACAAAGCC 180
DB 561 CAGTCTTCAGGAGGCTCTGAGTGGCTGGCACAATTACTGGGATGATGACAAAGCC 620
QY 181 TATTAACCATCCCTGAAAGAGCCGCTTACAAATCTCCAGAGATACCTCCAGAACAGGTA 240
DB 621 TACAAATCCATCTGAAAGAGCCGCTTACAAATCTCCAGAGATACCTCCAGAACAGGTA 680
QY 241 TTCTCTAAGATCACCAGTGTGACACTCGAGATACCTGCAATCTGCTGCTGGAAG 300
DB 681 TTCTCTAAGATCACCAGTGTGACACTCGAGATACCTGCAATCTGCTGCTGGAAG 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTGAAGAACCTCAGTCAAGCTC 357
DB 741 GGGGCTACGAGGATATAGTGTGAGCTTGTATTACTGGGGCCACGAGATCATGTGCACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

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Tue Jul 15 10:45:09 2003

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Page 1

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OM nucleic - nucleic search, using sw model

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(without alignments)
3795.863 Million cell updates/sec

Title: US-09-759-112A-5

Perfect score: 363
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:

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7: /cgn2.6/ptodata/2/pubpna/US08_NEM_PUB.seq.*
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11: /cgn2.6/ptodata/2/pubpna/US10_NEM_PUB.seq.*
12: /cgn2.6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2.6/ptodata/2/pubpna/US60_NEM_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	363	100.0	363	US-09-759-112A-6	Sequence 6, Appl1
3	313.4	86.3	483	US-09-879-461-3	Sequence 3, Appl1
4	311.8	85.9	423	US-09-879-461-9	Sequence 9, Appl1
5	299	82.4	369	US-09-995-529-11	Sequence 11, Appl1
6	284.4	78.3	465	US-09-881-823-7	Sequence 7, Appl1
7	250.8	69.1	812	US-10-195-752-16	Sequence 16, Appl1
8	250.8	69.1	812	US-10-265-713-1	Sequence 1, Appl1
9	250.8	69.1	812	US-09-764-304-1	Sequence 15, Appl1
10	179.2	49.4	288	US-09-995-529-15	Sequence 69, Appl1
11	178.6	49.2	684	US-09-972-656-69	Sequence 83, Appl1
12	172	47.4	684	US-09-972-656-83	Sequence 11, Appl1
13	171	47.1	423	US-08-879-461-11	Sequence 11, Appl1
14	168.4	46.4	646	US-08-736-457-1113	Sequence 1113, Ap
15	168.4	46.4	646	US-09-902-941-1113	Sequence 1113, Ap
16	168.4	46.4	646	US-09-849-526-1113	Sequence 1113, Ap
17	168.4	46.4	646	US-10-017-754-1113	Sequence 1113, Ap
18	165	45.5	714	US-08-940-544-4	Sequence 4, Appl1
19	163.2	45.0	378	US-09-740-002-15	Sequence 15, Appl1

20	163.2	45.0	1428	10	US-09-740-002-19	Sequence 19, Appl1
21	160.2	44.1	454	9	US-09-797-941A-1	Sequence 1, Appl1
22	158.8	43.7	378	10	US-09-740-002-13	Sequence 13, Appl1
23	158.8	43.7	1428	10	US-09-740-002-17	Sequence 17, Appl1
24	156.8	43.2	10517	9	US-10-059-261-1	Sequence 1, Appl1
25	156.6	43.1	5079	10	US-09-809-517A-41	Sequence 41, Appl1
26	156	43.0	750	10	US-09-730-374-1	Sequence 251, App
27	153.8	42.4	369	9	US-10-207-655-251	Sequence 267, App
28	152.8	42.1	1683	9	US-10-207-655-267	Sequence 253, App
29	152.8	42.1	825	9	US-10-207-655-253	Sequence 36, Appl1
30	148.2	40.8	351	9	US-10-153-401-36	Sequence 3, Appl1
31	147.8	40.7	458	9	US-09-990-205-3	Sequence 65, Appl1
32	147.8	40.7	458	10	US-10-153-401-65	Sequence 7, Appl1
33	147.8	40.7	814	9	US-08-779-784-7	Sequence 3, Appl1
34	147.2	40.6	417	7	US-08-779-784-7	Sequence 3, Appl1
35	145.6	40.1	360	9	US-10-232-187-1	Sequence 36, Appl1
36	145.6	40.1	420	10	US-09-007-093-3	Sequence 35, Appl1
37	143.8	39.6	4145	9	US-10-001-934-36	Sequence 37, Appl1
38	143.8	39.6	5020	9	US-10-001-934-35	Sequence 35, Appl1
39	142.6	39.3	454	10	US-09-881-823-3	Sequence 354, App
40	139.8	38.5	518	10	US-10-207-655-354	Sequence 35, App
41	139.6	38.5	366	9	US-10-207-655-353	Sequence 356, App
42	139.6	38.5	423	10	US-09-742-693-29	Sequence 357, App
43	138.6	38.2	734	10	US-10-207-655-356	Sequence 357, App
44	138.6	38.2	825	9	US-10-207-655-357	Sequence 357, App
45	138.6	38.2	1536	9	US-10-207-655-357	Sequence 357, App

ALIGNMENTS

RESULT 1
US-09-759-112A-5
Sequence 5, Appl1 Application US/09759112A
Publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Helmut
TITLE OF INVENTION: NOCORTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT CHAIN ANTIBODIES
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTING WITH THE C-TERMINAL REGION OF THE HEAVY CHAIN OF THE 1F7 ANTIBODY
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759, 112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 363
TYPE: DNA
ORGANISM: mouse
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(362)
OTHER INFORMATION: 1F7 VH chain gene
US-09-759-112A-5
Query Match 100.0%; Score 363; DB 9; Length 363;
Best Local Similarity 100.0%; Pred. No. 9.7e-114; Mismatches 0; Gaps 0;
Matches 363; Conservative 0; Indels 0;
1 CAGGTACTCTGAAGAAGTCTGGCCCTGGATATGACAGCCCTCCAGACCTCAAGCTG 60
|||||
1 CAGGTACTCTGAAGAAGTCTGGCCCTGGATATGACAGCCCTCCAGACCTCAAGCTG 60
61 ACTGTTCTTCTCTGGGTTTCACTGACACTTGTGATGGGCTGAGCTGATGCA 120
|||||
61 ACTGTTCTTCTCTGGGTTTCACTGACACTTGTGATGGGCTGAGCTGATGCA 120
121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGACACATTTACTGGATGATGACAAGCC 180
|||||
121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGACACATTTACTGGATGATGACAAGCC 180
181 TATACCCATCCCTGAAGAGCGGCTTACATCTCCAGATACCTCCAGACACAGGTA 240
|||||

Db 181 TATTAACCATCCCTGAAGAGCCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
Qy 241 TTCCCTAAGATCACCAGCTGTGACACTGAGATCTGCGACATCTACTGTCTGGAAG 300
Db 241 TTCCCTAAGATCACCAGCTGTGACACTGAGATCTGCGACATCTACTGTCTGGAAG 300
Qy 301 GTCTCTTAAGTCCCTATCTATGAGTACTGGGGTCAAGAACTCAAGCTCCTCC 360
Db 301 GTCTCTTAAGTCCCTATCTATGAGTACTGGGGTCAAGAACTCAAGCTCCTCC 360
Qy 361 TCA 363
Db 361 TCA 363

RESULT 2
US-09-759-112A-6
Sequence 6, Application US/09759112A
Publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Sybille
INVENTOR: Kohler, Heinz
TITLE OF INVENTION: NOCLECTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 363
TYPE: DNA
ORGANISM: mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(363)
OTHER INFORMATION: 1F7 VH chain gene
US-09-759-112A-6

Query Match 100.0%; Score 363; DB 9; Length 363;
Best Local Similarity 100.0%; Pred. No. 9.7e-114;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTTACTCTGAAGAGCTGTGCGCTGGGATTTTCAGACCCCTCCAGACCTCAGTCTG 60
Db 1 CAGGTTACTCTGAAGAGCTGTGCGCTGGGATTTTCAGACCCCTCCAGACCTCAGTCTG 60
Qy 61 ACTTGTCTTCTCTGCGCTTTTCACTGACACTTCTGTATGGGTGTGAGCTGATTTGA 120
Db 61 ACTTGTCTTCTCTGCGCTTTTCACTGACACTTCTGTATGGGTGTGAGCTGATTTGA 120
Qy 121 CAGCCTTCAGGAAGAGGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAGCC 180
Db 121 CAGCCTTCAGGAAGAGGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAGCC 180
Qy 181 TATAACCATCCCTGAAGAGCCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
Db 181 TATAACCATCCCTGAAGAGCCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
Qy 241 TTCCCTAAGATCACCAGCTGTGACACTGAGATCTGCGACATCTACTGTCTGGAAG 300
Db 241 TTCCCTAAGATCACCAGCTGTGACACTGAGATCTGCGACATCTACTGTCTGGAAG 300
Qy 301 GTCTCTTAAGTCCCTATCTATGAGTACTGGGGTCAAGAACTCAAGCTCCTCC 360
Db 301 GTCTCTTAAGTCCCTATCTATGAGTACTGGGGTCAAGAACTCAAGCTCCTCC 360
Qy 361 TCA 363
Db 361 TCA 363

RESULT 3
US-09-879-461-3
Sequence 3, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
INVENTOR: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/879,461
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-Oct-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-879-461-3

Query Match 86.3%; Score 313.4; DB 9; Length 483;
Best Local Similarity 91.5%; Pred. No. 8.8e-97;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGGTTACTCTGAAGAGCTGTGCGCTGGGATTTTCAGACCCCTCCAGACCTCAGTCTG 60
Db 1 CAGGTTACTCTGAAGAGCTGTGCGCTGGGATTTTCAGACCCCTCCAGACCTCAGTCTG 60
Qy 61 ACTTGTCTTCTCTGCGCTTTTCACTGACACTTCTGTATGGGTGTGAGCTGATTTGA 120
Db 61 ACTTGTCTTCTCTGCGCTTTTCACTGACACTTCTGTATGGGTGTGAGCTGATTTGA 120
Qy 121 CAGCCTTCAGGAAGAGGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAGCC 180
Db 121 CAGCCTTCAGGAAGAGGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAGCC 180
Qy 241 CAGCCTTCAGGAAGAGGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAGCC 300
Db 241 CAGCCTTCAGGAAGAGGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAGCC 300
Qy 301 TATAACCATCCCTGAAGAGCCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
Db 301 TATAACCATCCCTGAAGAGCCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240

Db 241 TTCTCAGATCACCAGTGTGGACACTGCAGATACCTCCACTTACTACTGTCTCGAGA 300
Oy 301 G-----TCTCTTAAGTCCCTATGCTATGAGTACTGGGTCAAGAACCTCAGTACC 354
Db 301 GCTAAGTATGTAAACCCCTACTATGATGAGTACTGAGGTGCAAGAACCTCAGTACC 360
Oy 355 GTCTCTCA 363
Db 361 GTCTCTCA 369

RESULT 6

US-09-881-823-7
; Sequence 7, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(441)
US-09-881-823-7

Query Match 78.3%; Score 284.4; DB 10; Length 465;
Best Local Similarity 88.0%; Pred. No. 6, Be-87;
Matches 322; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Oy 1 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACAGCCCTCCAGACCTCAGTCTG 60
Db 70 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACAGCCCTCCAGACCTCAGTCTG 129
Oy 61 ACTTGTCTTCTCTGTGGTTTTCAGTACGACTTCTGTGTGAGTGTGAGTGTGCA 120
Db 130 ACTTGTCTTCTCTGTGGTTTTCAGTACGACTTCTGTGTGAGTGTGAGTGTGCA 189
Oy 121 CAGCCTTCAGGAAGGCTGTGAGTGTGACGACACATTTACTGGATGTGACAAACGCG 180
Db 190 CAGCCTTCAGGAAGGCTGTGAGTGTGACGACACATTTACTGGATGTGACAAACGCG 249
Oy 181 TATAACCATCCCTGAAGACCGGCTTACAATCTCCAAGATACTTCCAGCAACAGTA 240
Db 250 TATAACCATCCCTGAAGACCGGCTTACAATCTCCAAGATACTTCCAGCAACAGTA 309
Oy 241 TTCTCTCAAGTACAGTGTGACACTGCGATATCTCCACATATCTACTGTCTCGAAG 300
Db 310 TTCTCTCAAGTACAGTGTGACACTGCGATATCTCCACATATCTACTGTCTCGAAG 369
Oy 301 GTCTCTCAAGTGTGAGTGTGACACTGCGATATCTCCACATATCTACTGTCTCGAAG 357
Db 370 GAGGGGGCTGCGGCTGAGTGTGATGAGTACTGAGGTCAAGAACTCTGATCACCCTC 429
Oy 358 TCCTCA 363
Db 430 TCCTCA 435

RESULT 7

US-10-195-752-16
; Sequence 16, Application US/10195752
; Publication No. US20030077276A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU

TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/195,752
FILING DATE: 16-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50

FEATURE:
NAME/KEY: TATA_signal
LOCATION: 261..267
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-195-752-16

Query Match 69.1%; Score 250.8; DB 9; Length 812;
Best Local Similarity 82.2%; Pred. No. 2, 3e-75;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

Oy 1 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACAGCCCTCCAGACCTCAGTCTG 60
Db 441 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACAGCCCTCCAGACCTCAGTCTG 500
Oy 61 ACTTGTCTTCTCTGTGGTTTTCAGTACGACTTCTGTGTGAGTGTGAGTGTGCA 120
Db 501 ACTTGTCTTCTCTGTGGTTTTCAGTACGACTTCTGTGTGAGTGTGAGTGTGCA 560
Oy 121 CAGCCTTCAGGAAGGCTGTGAGTGTGACGACACATTTACTGGATGTGACAAACGCG 180
Db 561 CAGTCTTCAGGAAGGCTGTGAGTGTGACGACACATTTACTGGATGTGACAAACGCG 620
Oy 181 TATAACCATCCCTGAAGACCGGCTTACAATCTCCAAGATACTTCCAGCAACAGTA 240
Db 621 TATAACCATCCCTGAAGACCGGCTTACAATCTCCAAGATACTTCCAGCAACAGTA 680
Oy 241 TTCTCTCAAGTACAGTGTGACACTGCGATATCTCCACATATCTACTGTCTCGAAG 300
Db 681 TTCTCTCAAGTACAGTGTGACACTGCGATATCTCCACATATCTACTGTCTCGAAG 740

[illegible]

US-09-/64-304-1

Query Match 69.18; Score 250.8; DB 10; Length 812.

Best Local Similarity 82.28; Pred. No. 2,3e-75;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1

QY	CAGGTTACTCTGAAAGAGTCGTGGCCCTGGGAATATTCGACGCCCTCCAGACCCCTCAGTCG	60
Db	441 CAGGTTACTCTGAAAGAAATCTGGCCCTGGGAATATTCGACGCCCTCCAGACCCCTCAGTCG	500
QY	61 ACTTGTCTCTTCTCTGGGTTTTCACGTAGCACTTCCTGGTATGGGTGTGAGCTGGATTGGA	120
Db	501 ACTTGTCTCTTCTCTGGGTTTTCTACTGAGCACTTATGTGTATGTGTGGGTGGATTGCT	560
QY	121 CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACAACATTTCTGGATGATGACAAAGCC	180
Db	561 CAGCTCTTCAGGGAAGGGTCTGGAGTGGCTGGCAAAAGTTTGGTGAAGTGAATGCTAAATAC	620
QY	181 TATTAACCCATCCCTGGAAGACCGGCTTTCATATCTCCAGATTTACTCTCAGCAATCAGGTA	240
Db	621 TACAAATCCATCTCTGAAAAACCGGCTCACAATTTCTCAAGGACACCTCCACAAACAGCA	680
QY	241 TTCCTCAAGATCACCAAGTGTGGACACTCGAGATATCTGCACATCTACTGTGTCGAAGG	300
Db	681 TTCCTCAAGATCACCAATATGGAACACTCGAGATATCTGCATATCTACTGTGCTGGGAGA	740
QY	301 GTTCTCTTAATGCTCTAATGCTA---TGGACTAATCTGGGCTCAAGAACCTAGTCAACCGTC	357
Db	741 GGGGCTACGAGAGGATATAGTGAAGCTTTGATTACTGTGGGCCACGAGATCATGTGTACAGTC	800
QY	358 TCCTCA 363	
Db	801 TCCTCA 806	

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RESULT 10
US-09-995-529-15
: Sequence 15, Application US/09995529
: Publication No. US20030096554.1
: GENERAL INFORMATION:
: APPLICANT: Watkins, Jeffrey D.
: APPLICANT: Huse, William D.
: APPLICANT: Tang, Ying
: TITLE OF INVENTION: Humanized Collagen Antibodies and
: FILE OF INVENTION: Related Methods
: FILE REFERENCE: P-IX 4976
: CURRENT APPLICATION NUMBER: US/09/995,529
: CURRENT FILING DATE: 2001-11-26
: NUMBER OF SEQ ID NOS: 358
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 15
: LENGTH: 288
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-995-529-15

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Query Match	49.48;	Score 179.2;	DB 9;	Length 288;
Best Local Similarity	-76.48;	Pred. No. 4.3e-51;		
Matches 220; Conservative	0;	Mismatches 68;	Indels 0;	Gaps 0;

[illegible]

OY		241	TTCCTCAAGATCACCAGTGTGGACACTGAGATACTGCCACATAC	288
Db		241	GTCCTTACAATGACCAACATGGAGCCCTGTGGACACAGCACGATATAC	288

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RESULT 11
US-09-972-656-69
Sequence 69, Application US/09972656
Publication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 69
LENGTH: 666
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(666)
US-09-972-656-69

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Query Match	49.28;	Score 178.6;	DB 9;	Length 666;
Best Local Similarity	70.88;	Pred. No. 9.2e-51;		
Matches 254;	Conservative	0;	Mismatches 99;	Indels 6;
				Gaps 1

QY	1	CAGGTACACCTGAAAAGCTGGCCCTGGGAATTGACGCCCTCCACAGCCTCAAGTCT	60
Db	1	CAGGTACACCTGAAAAGCTGGCTCTGTGCTGGTGAATCCACAGAGACCTTCACGCTG	60
QY	61	ACTGTGTCCTTCTCTGGGTTTTCAGTAGACACTTGGTATGGGTGAGCTGATTGCA	120
Db	61	ACCTGGACCGTGTCTGGGTTTCTCACTGACCAATGCTAAATGGGTGTGATGGATCCGT	120
QY	121	CAGCCTTACAGAAAGGCTGGAGAGGCGTCGACACATTTACTGGGAATGATGACAAGCG	180
Db	121	CAGCCCCCAAGGAAGGCCCTGGAGTGGCTGTCACACATTTTTTGGATAGCAAGAAATCC	180
QY	181	TATTAACCCATCCCTGAGAGCCGGCTTACATCTCCAAAGATTCCCTCAGCAACAGTA	240
Db	181	TACAGACATCTCTGTAAGACAGGGTCAACCACTCCAAAGACACTCCAAAGCCAGGTG	240
QY	241	TTTCCTCAAGATCACACAGTGTGGACACTGAGATTAATGCAATACTACTGTGCTGGAAG	300
Db	241	GTCCTTACCATGACCAACATGACCTGTGGACACAGGCAGGTATTACTGTGACAG----	296
QY	301	GTCCTCTTAACGCCATATCTTAATGACATCTAGGGGTCAAGAACCTCAGTACCGCTTC	359
Db	297	--GCTTTTATGTACAGAGGGTTTCACACCCCTGGGGCCAGGAAACCTGTGATACCGTCTC	353

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: RESULT 12
: US-09-972-656-83
: Sequence 83, Application US/09972656
: Publication No. US20030099647A1
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: APPLICANT: Tsai, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: TITLE OF INVENTION: Neutralizing Activity
: FILE REFERENCE: A-799
: CURRENT APPLICATION NUMBER: US/09/972,656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 83
:
: LENGTH: 684

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(684)
US-09-972-656-83

Query Match 47.4%; Score 172; DB 9; Length 684;
Best Local Similarity 69.4%; Pred. No. 1.7e-48;
Matches 254; Conservative 0; Mismatches 100; Indels 12; Gaps 1;

QY 6 TACTCTGAAGAGCTGGCCCTGGGATTTGACACCCCTCCAGACCCCTCACTGACTTG 65
DB 6 TACCTTGAGAGCTGCTCTACCTGCTGCTCAACCCGACACACCCCTCAGCTGACCTG 65
QY 66 TTCTTCTGCTGCTTTCACGACACTCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTG 125
DB 66 CTCTCTGCTGCTGCTTCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 125
QY 126 TTCAGAAAGGCTGAGTGGCTGACACATTTACTGAGATGATGACAGCGCTATTA 185
DB 126 CCCAGAAAGGCCCCGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
QY 186 CCCATCCCTGAAGACCGGCTTACATCTCCAGAGATCTCCAGCAACGATTTCT 245
DB 186 CCCCTCTGAGAGACAGCTCATCTGTTAACAGAGACCTCCAAAGCCAGGTTGCT 245
QY 246 CAATATCACAGTGTGACATCTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
DB 246 TACATATCACAAATGACCTGCTGACACGCGCCACATATTTGCTGACACACATCTG 305
QY 306 TCTACTG-----CCTATGCTATGACTACTGAGGCTCAAGAACCTCAGTAC 353
DB 306 CAGATATGCTGCTACTCAACGCGGTGTTTGTATGCTGCTGCGCCAGAGGACAGGCTAC 365
QY 354 CGTCTC 359
DB 366 CGTCTC 371

RESULT 13
US-09-879-461-11
Sequence 11, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-879-461-11

Query Match 47.1%; Score 171; DB 9; Length 423;
Best Local Similarity 66.9%; Pred. No. 3.1e-48;
Matches 243; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 CAGGTACTCTGAAGAGCTGGCCCTGGGATTTGACAGCCCTCCAGACCCCTCACTG 60
DB 61 CAGGTACTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 61 ACTGTTCTTCTGCTGCTTTCACCTGACACTTCTGCTATGCTGCTGCTGCTGCTGCT 120
DB 121 ACTGCACTCTCTCGGCTTCTCCCTGTCACCTCCGCTATGCTGCTGCTGCTGCTGCT 180
QY 121 CAGCTTCAGAAAGGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 181 CAGCGCGCGGTAAAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 181 TATACCCATCCCTGAAGAGCGGCTTACATCTCCAGAGATCTCCAGCAACGAGTA 240
DB 241 TACAAACCGAGCTGAATATCCGCTGACGATATCCAAAGACCTCCGTAACAGGTT 300
QY 241 TTCCTCAAGATCACAGTGTGACACTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 301 GTTCTGACATGACTTACATGACCGCGTTGACACCGCTACTACTGCTGCTGACGC 360
QY 301 GTCCTCTAAGTGTGCTATGATGACCTGACCTGAGGCTGTAAGAACTGCTGACGCTCC 360
DB 361 GAAACCGTTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 361 TCA 363
DB 421 TCA 423

RESULT 14
US-09-736-457-1113
Sequence 1113, Application US/09736457
Patent No. US2002016837A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Reiter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13

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RESULT 15
US-09-902-941-1113
: Sequence 1113, Application US/09902941
: Patent No. US20020172952A1
: GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Ranger, Darrick
APPLICANT: Ronger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF LUNG CANCER
: FILE REFERENCE: 210121.478617
: CURRENT APPLICATION NUMBER: US/09/902,941
: CURRENT FILING DATE: 2001-07-10
: NUMBER OF SEQ. ID NOS: 2002
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1113
: LENGTH: 646
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:

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Search completed: July 10, 2003, 22:17:40
Job time : 154 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 22:13:44 ; Search time 1741 Seconds
(without alignments)
3376.773 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagatgc.....ccctcagtcacgtctcctca 363

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_estbm: *
3: em_estln: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estm: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rdg: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302.6	83.4	864	10	BE309336 601093720
2	300.6	82.8	913	12	BF583109 602098016
3	298.6	82.3	666	13	BG963642 602828443
4	295.8	81.3	940	12	BF178694 601806679
5	292.6	80.6	947	14	BQ943210 AGENCOURT
6	281.4	77.5	652	13	BG963304 602827722

7	278	76.6	391	10	AM989547 u914h06.y
8	271.6	74.8	920	14	BQ231128 AGENCOURT
9	267.6	73.7	379	10	BB872138 BB872138
10	262.6	72.3	363	10	BB870162 BB870162
11	262.4	72.3	366	10	BB870127 BB870127
12	260.6	71.8	438	9	AA880491 AA880491
13	259.8	71.6	900	12	BF581194 602100390
14	259.6	71.5	377	10	BB873796 BB873796
15	259.6	71.5	589	17	AZ882936 RCT-23-1
16	254.2	70.0	920	12	BF580719 602093665
17	253.4	69.8	920	10	BE289865 601088740
18	243.6	67.1	374	10	BB868022 BB868022
19	237	65.3	769	12	BF582574 602094551
20	234.8	64.7	340	10	BB869851 BB869851
21	224	61.7	330	10	BB870527 BB870527
22	207.8	57.2	827	13	BM007964 603617691
23	206.2	56.8	904	12	BG758540 602712758
24	200.6	55.3	311	9	A1466485 vx40h05.y
25	196.6	54.2	941	14	BQ707283 BQ707283
26	196.6	54.2	945	14	BQ708104 BQ708104
27	195	53.7	1083	13	B1762661 B1762661
28	191.8	52.8	384	10	BE246586 TCBAPIE49
29	191.8	52.8	385	10	BE247351 TCBAPIE34
30	191.6	52.8	923	12	BF663900 602145560
31	190.2	52.4	439	10	BE247437 TCBAPIE63
32	189	52.1	955	14	BQ711772 BQ711772
33	189	52.1	956	14	BQ709744 BQ709744
34	188.2	51.8	955	12	BF238095 601811815
35	186.8	51.5	324	10	BB872886 BB872886
36	186.8	51.5	620	14	BM788928 K-EST0068
37	186.2	51.3	953	14	BQ709902 AGENCOURT
38	183.2	50.5	432	10	AM630601 h81h12.y
39	181	49.9	783	12	BG340576 602462145
40	180.6	49.8	924	12	BG756803 602710276
41	179.6	49.5	931	12	BF663492 602144657
42	179	49.3	955	14	BQ878660 AGENCOURT
43	177.8	49.0	674	14	BM691116 UI-E-C11-
44	176.6	48.7	761	13	BM008301 603617958
45	176.6	48.7	801	13	BM008059 603617825

ALIGNMENTS

RESULT 1
BE309336 864 bp mRNA linear EST 26-OCT-2000
LOCUS 601093720F1 NCI CGAP Mam5 Mus musculus cDNA clone IMAGE:3488309 5',
DEFINITION mRNA sequence.
ACCESSION BE309336
VERSION BE309336.1 GI:9167366
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1. (bases 1 to 864)
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LAM8527 row: h column: 06
High quality sequence stop: 645.
Location/Qualifiers

FEATURES
source

1. 864

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_1lb="NCI CGAP Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lotmar Hemmighausen/Robin Humphreys, NIH"
BASE COUNT      171 a      222 g      211 t
ORIGIN

Query Match      83.4%; Score 302.6; DB 10; Length 864;
Best Local Similarity 92.2%; Pred. No. 1.3e-82;
Matches 344; Conservative 0; Mismatches 19; Indels 10; Gaps 2;

1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
43 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 102
61 ACTTGTTCCTCTCTGGGTTTTCACAGCACTCTGTGTGTGTGTGTGTGTGTGTGTG 119
103 ACTTGTTCCTCTCTGGGTTTTCACAGCACTCTGTGTGTGTGTGTGTGTGTGTGTG 162
120 ACAGCCTTCAGAAAGGCTGTGGAGTGTGGACACATTTACTGGGATGATACAAAGC 179
163 TCAGCCTTCAGAAAGGCTGTGGAGTGTGGACACATTTACTGGGATGATACAAAGC 222
180 CTATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGATACCTCCAGCAACAGT 239
223 CTATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGATACCTCCAGCAACAGT 282
240 ATTCTCTGAGATACCAAGTGTGACACTGAGATCTGCCACATCTACTGTCTGTGAAG 299
283 ATTCTCTGAGATACCAAGTGTGACACTGAGATCTGCCACATCTACTGTCTGTGAAG 342
300 GGTCTCTCTACTG-----CTATGCTATGACTACTGGGGTCAAGAACCTCAGT 350
343 TTATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGATACCTCCAGCAACAGT 402
DB
QY 351 CACCGTCTCTCTCA 363
DB 403 CACCGTCTCTCTCA 415

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RESULT 2
583109 913 bp mRNA linear EST 12-DEC-2000
LOCUS 602098016F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4218099 5',
DEFINITION mRNA sequence.
ACCESSION BF583109
VERSION BF583109.1 GI:11656827
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
1 (bases 1 to 913)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LIAM9797 row: p column: 04
High quality sequence stop: 656.
Location/Qualifiers
1. 913
/organism="Mus musculus"
/db_xref="FVB/N"
/db_xref="taxon:10090"
/clone_1lb="NCI CGAP Co24"
/lab_host="DH10B (rtI phage-resistant)"
/Note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      183 a      261 c      250 g      219 t
ORIGIN

Query Match      82.8%; Score 300.6; DB 12; Length 913;
Best Local Similarity 90.5%; Pred. No. 5.5e-82;
Matches 334; Conservative 0; Mismatches 29; Indels 6; Gaps 1;

1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
60 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 119
61 ACTTGTTCCTCTCTGGGTTTTCACAGCACTCTGTGTGTGTGTGTGTGTGTGTGTG 120
120 ACTTGTTCCTCTCTGGGTTTTCACAGCACTCTGTGTGTGTGTGTGTGTGTGTGTG 179
121 CACCGTTCAGAAAGGCTGTGGAGTGTGGACACATTTACTGGGATGATACAAAGC 180
180 CACCGTTCAGAAAGGCTGTGGAGTGTGGACACATTTACTGGGATGATACAAAGC 239
181 TATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGATACCTCCAGCAACAGT 240
240 TATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGATACCTCCAGCAACAGT 299
241 TTCTCTGAGATACCAAGTGTGACACTGAGATCTGCCACATCTACTGTCTGTGAAG 296
300 TTCTCTGAGATACCAAGTGTGACACTGAGATCTGCCACATCTACTGTCTGTGAAG 359
297 --AAGGCTCTCTTAACTGCTATGCTATGACTACTGGGGTCAAGAACCTCAGTACC 354
360 TATGATGCTTACCATATTTACTATGCTGTGACTGAGTGGGGTCAAGAACCTCAGTACC 419
DB
QY 355 GTCTCTCTCA 363
DB 420 GTCTCTCTCA 428

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RESULT 3
BG963642 666 bp mRNA linear EST 12-JUN-2001
LOCUS 602828443F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983155 5',
DEFINITION mRNA sequence.
ACCESSION BG963642
VERSION BG963642.1 GI:14351279
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
1 (bases 1 to 666)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LHAM0987 row: e column: 12
 High quality sequence stop: 658.
 Location/Qualifiers

FEATURES

source

1.666
 /organism="Mus musculus"
 /strain="FVB/N"
 /db.xref="taxon:10090"
 /clone="IMAGE:498315"
 /clone_lib="NCI_CGAP_C024"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: PCMV-SPORT6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."
 Technology: Note: this is a NCI_CGAP library.

BASE COUNT 157 a 186 c 159 g 164 t
 ORIGIN

Query Match

Best Local Similarity 82.3%; Score 298.6; DB 13; Length 666;
 Matches 343; Conservative 0; Mismatches 19; Indels 13; Gaps 2;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
 Db 59 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 117
 QY 61 ACTGTCT 120
 Db 118 ACTGTCT 177
 QY 121 CAGCCTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAAGCGC 180
 Db 178 CAGCCTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAAGCGC 237
 QY 181 TATAACCATCCCTGAAGAGCCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 240
 Db 238 TATAACCATCCCTGAAGAGCCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 297
 QY 241 TTCTCTCAAGATCAGCATGTGGACATCTGAGATCTGCCATATCTACTGTGCTCG--- 296
 Db 298 TTCTCTCAAGATCAGCATGTGGACATCTGAGATCTGCCATATCTACTGTGCTCGTAC 357
 QY 297 -----AAGGCTCTCTACTGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 348
 Db 358 TATAGTACTACTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
 QY 349 GTCACCGTCTCTCA 363
 Db 418 GTCACCGTCTCTCA 432

RESULT 4

BF178694

LOCUS 60180679F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4037587 5',
 DEFINITION mRNA sequence.

ACCESSION

BF178694

VERSION 1
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 940)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Lotmar Hennighausen Ph.D., Robin Humphreys
 CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LHAM314 row: n column: 20
 High quality sequence stop: 631.
 Location/Qualifiers

FEATURES

source

1.940
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db.xref="taxon:10090"
 /clone="IMAGE:4037587"
 /clone_lib="NCI_CGAP_Mam5"
 /tissue_type="tumor; gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site:1; SalI; Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lotmar Hennighausen/Robin Humphreys, NIH"
 NIH

BASE COUNT 206 a 267 c 259 g 207 t 1 others
 ORIGIN

Query Match

Best Local Similarity 81.5%; Score 295.8; DB 12; Length 940;
 Matches 331; Conservative 0; Mismatches 32; Indels 6; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
 Db 58 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 117
 QY 61 ACTGTCT 120
 Db 118 ACTGTCT 177
 QY 121 CAGCCTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAAGCGC 180
 Db 178 CAGCCTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGATGACAAAGCGC 237
 QY 181 TATAACCATCCCTGAAGAGCCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 240
 Db 238 TATAACCATCCCTGAAGAGCCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 297
 QY 241 TTCTCTCAAGATCAGCATGTGGACATCTGAGATCTGCCATATCTACTGTGCTCGAAG 300
 Db 298 TTCTCTCAAGATCAGCATGTGGACATCTGAGATCTGCCATATCTACTGTGCTCGAAG 357
 QY 297 -----CTATGCTATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 354
 Db 358 CGGTACTACTGCTCTTACTATGCTTTGGACATCTGAGTGGTGGTGGTGGTGGTGGTGG 417
 QY 355 GTCCTCTCA 363
 Db 418 GTCCTCTCA 426

RESULT 5

B0943210

LOCUS 8836910 NCI_CGAP_C024 Mus musculus cDNA clone
 DEFINITION IMAGE:6398059 5', mRNA sequence.

ACCESSION

B0943210

VERSION 1
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 947)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13896 row: 0 column: 20
High quality sequence stop: 669.

FEATURES

source
Location/Qualifiers
1. 947
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:6398059
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORE; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT
ORIGIN
218 a 272 c 235 g 221 t 1 others

Query Match
Best Local Similarity 87.9%; Score 292.6; DB 14; Length 947;
Matches 319; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 CAGTTACTGTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
DB 72 CAGTTACTGTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 131
QY 61 ACTGTCTTCTCTCTGGGTTTTCAGTACGACTTCTGTAGGTTGTGAGCTGGATTGCA 120
DB 132 ACTGTCTTCTCTCTGGGTTTTCAGTACGACTTCTGTAGGTTGTGAGCTGGATTGCA 191
QY 121 CAGCCTTCAGGAAGAAGGCTGAGAGTGGCTGGACACATTACTGAGTATGACAAAGCCG 180
DB 192 CAGCCTTCAGGAAGAAGGCTGAGAGTGGCTGGACACATTACTGAGTATGACAAAGCCG 251
QY 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
DB 252 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 311
QY 241 TTCTCTAAGATCAACCACTGTGGACACTGAGATACCTCCATACCTACTGTGCTCGAAG 300
DB 312 TTCTCTAAGATCAACCACTGTGGACACTGAGATACCTCCATACCTACTGTGCTCGAATA 371
QY 301 GTCTCTACTACTGCTATGATGACTACTGAGGTCAGAACTCAGTACAGCTCC 360
DB 372 AGGATAGTAACTACTGATCTGATGCTGGGGCCGACAGGACAGGTCACCGTCTCC 431
QY 361 TCA 363
DB 432 TCA 434

RESULT 6
LOCUS BG963304 652 bp mRNA linear EST 12-JUN-2001
DEFINITION 602827722F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982549 5',
ACCESSION BG963304
VERSION BG963304.1 GI:14350941
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 652)
Mammalia: Eutheria, Rodentia, Sclurognathia: Muridae, Murinae, Mus.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10985 row: 1 column: 06
High quality sequence stop: 648.

FEATURES

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Location/Qualifiers
1. 652
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:4982549
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORE; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT
ORIGIN
141 a 184 c 163 g 164 t

Query Match
Best Local Similarity 77.5%; Score 281.4; DB 13; Length 652;
Matches 312; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 CAGTTACTGTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
DB 53 CAGTTACTGTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 112
QY 61 ACTGTCTTCTCTCTGGGTTTTCAGTACGACTTCTGTAGGTTGTGAGCTGGATTGCA 120
DB 113 ACTGTCTTCTCTCTGGGTTTTCAGTACGACTTCTGTAGGTTGTGAGCTGGATTGCA 172
QY 121 CAGCCTTCAGGAAGAAGGCTGAGAGTGGCTGGACACATTACTGAGTATGACAAAGCCG 180
DB 173 CAGCCTTCAGGAAGAAGGCTGAGAGTGGCTGGACACATTACTGAGTATGACAAAGCCG 232
QY 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 240
DB 233 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGATACCTCCAGCAACAGGTA 292
QY 241 TTCTCTAAGATCAACCACTGTGGACACTGAGATACCTCCATACCTACTGTGCTCGAAG 300
DB 293 TTCTCTAAGATCAACCACTGTGGACACTGAGATACCTCCATACCTACTGTGCTCGATTG 352
QY 301 GTCTCTACTACTGCTATGATGACTACTGAGGTCAGAACTCAGTACAGCTCC 360
DB 353 CCTATTATTTGCTATTGTGATCTGATGCTGGGGCCGACAGGACAGGTCACCGTCTCC 412
QY 361 TCA 363
DB 413 TCA 415

RESULT 7
LOCUS AW989547 391 bp mRNA linear EST 02-JUN-2000
DEFINITION u91406.v1 Soares_mammary_gland_NIMMG Mus musculus cDNA clone
IMAGE:1351643 5' similar to SW:HV28.HUMAN P04438 IG HEAVY CHAIN
V-JI REGION SESS PRECURSOR. [1]; mRNA sequence.
ACCESSION AW989547
VERSION AW989547.1 GI:8184975
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 391)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 TITLE Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MG1:947743
 Trace considered overall poor quality
 Seq primer: -40RP from Glibco
 High quality sequence stop: 1.

FEATURES

Source

1. 391
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1531643"
 /clone_lib="Soares_mammary_gland_NMLMG"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Benito Soares and M. Fatima Bonaldo."

BASE COUNT

88 a 107 c 90 g 106 t

ORIGIN

Query Match 76.6%; Score 278; DB 10; Length 391;
 Best Local Similarity 95.0%; Pred. No. 3.9e-75;
 Matches 287; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 CAGGTACTCGAAGAAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAAGTCTG 60
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 DB 56 CAGGTACTCGAAGAAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAAGTCTG 115
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 QY 61 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGAGTTCGA 120
 |||||||
 DB 116 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGAGTTCGT 175
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 QY 121 CAGCCTTCAGAAAGGCTGAGTGGCTGGACACATTTACTGGATGATGACAGCGC 180
 |||||||
 DB 176 TAGCCTTCAGAAAGGCTGAGTGGCTGGACACATTTACTGGATGATGACAGCGT 235
 |||||||
 QY 181 TATTAACCATCCCTGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACAGGTA 240
 |||||||
 DB 236 TATTAACCATCCCTGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACAGGTA 295
 |||||||
 QY 241 TTCCTCAAGATCAGCAGTGTGAGACATGAGATACCTCAATCTACTGAGTGAAG 300
 |||||||
 DB 296 TTCCTCAAGATCAGCAGTGTGAGACATGAGATACCTCAATCTACTGAGTGAAGC 355
 |||||||
 QY 301 GT 302
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 DB 356 GT 357

RESULT 8
 BQ231128 920 bp mRNA linear EST 02-MAY-2002
 LOCUS AGENCOURT.7578094 NCI CGAP.St1 Mus musculus cDNA clone
 DEFINITION IMAGE:6051673 5', mRNA sequence.
 ACCESSION BQ231128
 VERSION BQ231128.1 GI:20412528
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 920)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LRAM1305 row: 0 column: 02
 High quality sequence stop: 640.

FEATURES

Source

1. 920
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:6051673"
 /clone_lib="NCI CGAP.St1"
 /lab_host="DH10B (T1-resistant)"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.77 kb. Library constructed by Life Technologies. Note: this is a NCI/CGAP library."

BASE COUNT

205 a 264 c 224 g 222 t

ORIGIN

Query Match 74.8%; Score 271.6; DB 14; Length 920;
 Best Local Similarity 85.8%; Pred. No. 5.1e-73;
 Matches 314; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 CAGGTACTCGAAGAAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAAGTCTG 60
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 QY 61 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGAGTTCGA 120
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 DB 91 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGAGTTCGT 150
 |||||||
 QY 121 CAGCCTTCAGAAAGGCTGAGTGGCTGGACACATTTACTGGATGATGACAGCGC 180
 |||||||
 DB 151 CAGCCTTCAGAAAGGCTGAGTGGCTGGACACATTTACTGGATGATGACAGCGT 210
 |||||||
 QY 181 TATTAACCATCCCTGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACAGGTA 240
 |||||||
 DB 211 TATTAACCATCCCTGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACAGGTA 270
 |||||||
 QY 241 TTCCTCAAGATCAGCAGTGTGAGACATGAGATACCTCAATCTACTGAGTGAAG 297
 |||||||
 DB 271 TTCCTCAAGATCAGCAGTGTGAGACATGAGATACCTCAATCTACTGAGTGAAGC 330
 |||||||
 QY 298 AGGCTCTCTCAACTGCTATGATGACATCTGAGGCTCAAGACACTGATCAGCTC 357
 |||||||
 DB 331 CGATGGTCACTTCTTATTTGATGATGAGTGTGGGCGAGGACACACGTCACGTC 390
 |||||||
 QY 358 TCCTCA 363
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 DB 391 TCCTCA 396

RESULT 9
 BB872138 379 bp mRNA linear EST 27-NOV-2001
 LOCUS BB872138
 DEFINITION BB872138 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630034P22 5', mRNA sequence.
 ACCESSION BB872138
 VERSION BB872138.1 GI:17118348
 KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 379)
AUTHORS Akimura,T., Arikawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Koude,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeku-Akhiba,S., Tanaka,T., Tomaru,A., Toya,T., Watanabe,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
TITLE Unpublished (2001)
JOURNAL Contact: Yoshinide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.
FEATURES
source
1. 379
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, adult male accessory axillary lymph node"
/sex="male"
/tissue_type="accessory axillary lymph node"
/dev_stage="adult"
/note="pooled tissues: (tissue_type=cerebellum, dev_stage=16 days neonate, sex=mixed), (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=adult), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"
BASE COUNT 84 a 97 c 93 g 105 t
ORIGIN
Query Match 73.7%; Score 267.6; DB 10; Length 379;
Best Local Similarity 93.6%; Pred. No. 6.3e-72;
Matches 279; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 CAGGTACTCTGAAAGAGCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGCTG 60
DB 79 CAGGTACTCTGAAAGAGCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGCTG 138

QY 61 ACTGTTCTTCTCTGGGTTTTCACAGCACTTCGTATGGGTGAGCTGATTCGA 120
DB 139 ACTGTTCTTCTCTGGGTTTTCACAGCACTTCGTATGGGTGAGCTGATTCGT 198
QY 121 CAGCCTTACGAAAGGCTCTGAGTGGCTGGCACATTTACTGGGATGATGACACAGCC 180
DB 199 CAGCCTTACGAAAGGCTCTGAGTGGCTGGCACATTTACTGGGATGATGATGATAC 258
QY 181 TATACCATCCCTGAGAGCCGCTTACATCTCCAGAGTACCTCCAGACAGGTA 240
DB 259 TATACCATCCCTGAGAGCCGCTTACATCTCCAGAGTACCTCCAGACAGGTA 318
QY 241 TTCCCTCAAGATCCAGCTGAGACACTGAGATATGCGACATATCTGCTCGAA 298
DB 319 TTCCCTCAAGATCCAGCTGAGACACTGAGATATCTGCTCGAA 376
RESULT 10
BB870162
LOCUS
DEFINITION
BB870162 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630018N20 5', mRNA sequence.
ACCESSION
BB870162
VERSION
BB870162.1 GI:17116372
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
REFERENCE
Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 363)
AUTHORS Akimura,T., Arikawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Koude,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeku-Akhiba,S., Tanaka,T., Tomaru,A., Toya,T., Watanabe,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
TITLE Unpublished (2001)
JOURNAL Contact: Yoshinide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.
FEATURES
source
1. 363
Location/Qualifiers


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/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="G630018N20"
/clone_lib="RIKEN full-length enriched, adult male
accessory axillary lymph node"
/sex="male"
/tissue_type="accessory axillary lymph node"
/dev_stage="adult"
/note="pooled tissues: (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"

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BASE COUNT 79 a 93 c 90 g 101 t

ORIGIN

Query Match 72.3% Score 262.6; DB 10; Length 363;
Best Local Similarity 93.5% Pred. No. 2.2e-70;
Matches 274; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 60
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QY 61 ACTTGTTCTTCTCTGCGTTTTCACATGACACTTCTGATGGGTGAGCTGATTCGA 120
DB 131 ACTTGTTCTTCTCTGCGTTTTCACATGACACTTCTGATGGGTGAGCTGATTCGT 190
QY 121 CAGCCTTCAGGAAAGGCTGAGAGTGGCTGGACACATTTACTGGATGATGACACGC 180
DB 191 CAGCCTTCAGGAAAGGCTGAGAGTGGCTGGACACATTTACTGGATGATGATGATAC 250
QY 181 TATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGTATCCTCCAGACACAGTA 240
DB 251 TATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGTATCCTCCAGACACAGTA 310
QY 241 TTCTCTAAGATCCCAATGTCGACATCGATCTCCACATCTACTGTCG 293
DB 311 TTCTCTAAGATCCCAATGTCGACATCGATCTCCACATCTACTGTCG 363

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RESULT 11
BB870127

LOCUS BB870127 366 bp mRNA linear EST 27-NOV-2001
DEFINITION BB870127 RIKEN full-length enriched, adult male accessory axillary
lymph node Mus musculus cDNA clone G630018I21 5', mRNA sequence.
BB870127
VERSION BB870127.1 GI:17116337
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 366)

REFERENCE

ATTNORS

Alimura, T., Arakawa, T., Carninci, P., Furuno, M., Hangaki, T.,
Hayasaka, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,
A., Takahashi, F., Takeku-Akehira, S., Tanaka, T., Tomaru, A., Toyata,
T., Watanabe, K., Yasunishi, A., Yamatsuta, M., and Hayashizaki, T.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
2001)

JOURNAL

COMMENT Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayasaka, N., Sugahara, Y., Shibata, K., Itoh,
M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
waghi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E.,
Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencing. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukushima, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers

1..366

/organism="Mus musculus"

/strain="C57BL/6J"

/db.xref="taxon:10090"

/clone="G630018I21"

/clone_lib="RIKEN full-length enriched, adult male
accessory axillary lymph node"

/sex="male"

/tissue_type="accessory axillary lymph node"

/dev_stage="adult"

/note="pooled tissues: (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"

BASE COUNT 80 a 94 c 91 g 101 t

ORIGIN

Query Match 72.3% Score 262.4; DB 10; Length 366;
Best Local Similarity 92.9% Pred. No. 2.5e-70;
Matches 275; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 60
DB 71 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 130
QY 61 ACTTGTTCTTCTCTGCGTTTTCACATGACACTTCTGATGGGTGAGCTGATTCGA 120
DB 131 ACTTGTTCTTCTCTGCGTTTTCACATGACACTTCTGATGGGTGAGCTGATTCGT 190
QY 121 CAGCCTTCAGGAAAGGCTGAGAGTGGCTGGACACATTTACTGGATGATGACACGC 180
DB 191 CAGCCTTCAGGAAAGGCTGAGAGTGGCTGGACACATTTACTGGATGATGATGATAC 250
QY 181 TATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGTATCCTCCAGACACAGTA 240
DB 251 TATTAACCATCCCTGAGAGCGGCTTACATCTCCAGAGTATCCTCCAGACACAGTA 310
QY 241 TTCTCTAAGATCCCAATGTCGACATCGATCTCCACATCTACTGTCG 296
DB 311 TTCTCTAAGATCCCAATGTCGACATCGATCTCCACATCTACTGTCG 366

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RESULT 12
AA880491

LOCUS AA880491 438 bp mRNA linear EST 26-MAR-1998

DEFINITION	ACCESSION VERSION	KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL	COMMENT
vx0h05.i1 Striatagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1277721 5' similar to gp.5659331_cds1 IG HEAVY CHAIN V-II REGION (HUMAN);, mRNA sequence.	AA880491 AA880491.1	GI:2989474	EST. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.	1 (bases 1 to 438) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Weisling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	The Mashu-HMI Mouse EST Project Unpublished (1996)	Contact: Marra M/Mouse EST Project

Email: mouseeat@atson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:669521
Seq primer: -28m13 rev1 ET from Amersham.

FEATURES
SOURCE

Location/Qualifiers
1. .438

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/clone_image="1277721"
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 sex="female"

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113	c
91	g
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Best Local Similarity	84.5%	Pred. No. 9.8e-70;	
Matches 305; Conservative	0;	Mismatches 54;	Indels 2;
			Gaps 1.

QY		1	CAGGTTACTGTGAAGAAGTCTGGCCCTGGGATATTGCAGGCCCTCCACACCCTCAGTCG	60
Db		80	CAGGTTACTGTGAAGAAGTCTGGCCCTGGGATATTGCAGGCCCTCCACACCCTCAGTCG	139
QY		61	ACTGTCCTTCTCTGGGGTTTCACTGAGCACTCTGGATGGGGTGAGCGGATTTGA	120
Db		140	ACTGTCCTTCTCTGGGGTTTCACTGAGCACTCTTAATCTGGGGTATAGCGTGGATTCGT	199
QY		121	CAGCCTTCAGGAAGGGCTCGAGTGGCTGGCACACATTTACTGGGATGATGACACGC	180
Db		200	CAGCCTTCAGGAAGGGCTCGAGTGGCTGGCACACATTTGGTGAATAAATGATAAAT	259
QY		181	TATTAACCATCCCTGGAAGAGCCGGCTTCATCTCCACAGGATTAACCTCAGGACAACG	240
Db		260	TATTAATCATCCCTGGAAGAGCCGATCATCTCCACAGGATTAATCCAACACACG	319
QY		241	TTCTCTCAAAGTACACCACTGTGGACACTGCAATACTGCCACATACTACTGTGCTG	300
Db		320	TTTCTCTCAAAGTACACCAATGTGTGATTCTACAAATCTGGCAGTACTGTGCTG	379

Oy 301 GTCCTCCTAACGCGCTATGCATTGGACCTAGTGGGGCAAGAACCCTACACCCGTCC 360
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Db 380 G--AAACTACGGTAGTGCTAGTTAGCTCTACTCTGGGGCCAAAGCACCTCTATCACAGTCTCC 437

Oy 361 T 361
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Db 438 T 438

RESULT 13

LOCUS	BF581194	900 bp	mus musculus	mus	musculus	CDNA clone	IMAGE:4220111	5'
DEFINITION	602100390F1 NCL_CGAP_Co24							
	MRNA sequence.							

ACCESSION	BF581194	
VERSION	BF581194.1	GI:11654906
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL *Genetics* 163:1-3 (2002).

JOURNAL COMMENT
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
E-mail: robert@strausberg.com

Tissue Procurement: Jeffrey E. Green, M.D.
Email: cgabpos-remail.nin.gov

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Data Generated by: The Institute for Genome Sciences and Policy

Clone distribution: MGC clone distribution information can be found through the T.M.A.C.M. Consortium (<http://www.tmacm.org>).

found through the I.M.A.V.E. Consortium/LEAD at:
http://image.llnl.gov
plate: ITAM0802 row: 3 column: 34

FFMMFMS
 F14AE: LHMMS005 LOW: C COLUMN: 24
 High quality sequence stop: 639.
 Location/Qualifiers

LENSONS	LOCATION/YEAR
SOURCE	1. 900
	/organism="Mus musculus"

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/organism="HVS_musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4220111"
/clone_id="NCI_CGAP_C024"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NCI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

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Query Match	71.6%;	Score 259.8;	DB 12;	Length 900;
Best Local Similarity	84.6%;	Pred. No. 2.3e-69;		
Matches 307; Conservative	0;	Mismatches 47;	Indels 9;	Gaps 1;

[illegible]

Db 296 TTCTGTGAAGATCCGACAGTGTGACACTGACAGATCTCCATATATATCTGTCTGCTG---- 351

QY 301 GTCTGTACTGCTGCTATGCTATGACTACTGGGGTCAAGAACCTCAGTCACCGCTCC 360

Db 352 -----CCGAAGTAACTGAGAGTTGACTACTGGGGCCAGGACCACTCAGTCACGCTCC 406

QY 361 TCA 363

Db 407 TCA 409

RESULT 14

BB873796 377 bp mRNA linear EST 27-NOV-2001

LOCUS BB873796 RIKEN full-length enriched, adult male accessory axillary

DEFINITION lymph node Mus musculus cDNA clone G630050003 5', mRNA sequence.

ACCESSION BB873796.1 GI:17120006

VERSION BB873796.1

KEYWORDS EST.

ORGANISM Mus musculus.

house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 377)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Matsuyama,T., Nakanura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

Unpublished (2001)

Contact: Yoshinide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagii,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

1..377

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="G630050003"

/clone_lib="RIKEN full-length enriched, adult male accessory axillary lymph node"

/sex="male"

/tissue_type="accessory axillary lymph node"

/dev_stage="adult"

/note="pooled tissues: (tissue_type=cerebellum, dev_stage=16 days neonate, sex=mixed), (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"

BASE COUNT 79 a 93 c 100 g 105 t

ORIGIN

Query Match 71.5%; Score 259.6; DB 10; Length 377;

Best Local Similarity 91.9%; Pred. No. 1,9e-69;

Matches 274; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db 69 CAGGTTACTGTGAAGAGTGTGGCCCTGGAGTATTCAGCCCTCCAGACCTCAGTCTG 128

QY 61 ACTTGTTCTTCTCTGCTTTTCTACTGACACTCTCTGTATGCTGTGACTGATCGA 120

Db 129 ACTTGTTCTTCTCTGCTTTTCTACTGACACTCTCTGTATGCTGTGACTGATCGT 188

QY 121 CAGCCTTCAGGAAAGGCTCTGAGTGTGCTGGCACACATTTACTGGATGATGACAAAGCG 180

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QY 181 TATTAACCATTCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGCACAGGTA 240

Db 249 TATTAACCATTCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAAAGAGGTA 308

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Db 309 TTCTGTGAAGATCCGACAGTGTGACACTGACAGATCTCCATATATCTGTCTGCTG 366

RESULT 15

AZ882936 589 bp DNA linear GSS 05-MAR-2001

LOCUS AZ882936

DEFINITION RPCI-23-187A23.TV RPCI-23 Mus musculus genomic clone RPCI-23-187A23

ACCESSION AZ882936

VERSION AZ882936.1 GI:13201881

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 589)

Zhao,S., Nierman,W., Feldbljum,T., Malek,J., Shatsman,S., Akiret B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSS: RPCI-23-187A23.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tftp/bac_ends/mouse/bac_end_intro.html

Plate: 187 row: A column: 23

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..589

FEATURES

source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_1b="RPCI-23-187A23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
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with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      142 a      160 c      123 g      164 t
ORIGIN
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Query Match      71.5%; Score 259.6; DB 17; Length 589;
Best Local Similarity 91.9%; Pred. No. 2.2e-69;
Matches 274; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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284 CAGGTTACTCTGAAGAGTCTGGCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 343
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344 ACTTGTCTCTTCTCTGGGTTTTCATGAGCATTCTGTATGGGTGTGAGCTGATTCGT 403
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Job time : 17/9 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:38:52 ; Search time 27 Seconds

(Without alignments)
131.858 Million cell updates/sec

Title: US-09-759-112A-7

Perfect score: 633
Sequence: 1 QVTLKESGPGTLPSPQTLSTL.....SLTAVAMDYMGQGTSTVYSS 121

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

262574

ALIGNMENTS

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

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- 2: /cg2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cg2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cg2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cg2_6/ptodata/1/1aa/PCUTS.COMB.pep:*
- 6: /cg2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	569	89.9	141	2	US-08-483-636-10	Sequence 10, Appl
4	569	89.9	141	2	US-08-483-632-10	Sequence 10, Appl
5	567.5	89.7	246	1	US-08-197-834-7	Sequence 7, Appl1
6	551.5	87.1	122	1	US-08-436-463-14	Sequence 14, Appl1
7	522.5	82.5	139	5	PCT-US95-07372-10	Sequence 10, Appl
8	521.5	82.4	120	2	US-08-553-501A-88	Sequence 88, Appl
9	521.5	82.4	120	3	US-09-205-231-88	Sequence 88, Appl
10	521.5	82.4	139	2	US-08-555-501A-29	Sequence 29, Appl
11	521.5	82.4	139	3	US-09-205-231-29	Sequence 29, Appl
12	506.5	80.0	120	2	US-08-290-592E-32	Sequence 32, Appl
13	505.5	79.9	143	1	US-08-436-463-2	Sequence 2, Appl1
14	504	79.6	108	1	US-08-436-463-17	Sequence 17, Appl
15	502	79.3	141	2	US-08-483-636-12	Sequence 12, Appl
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17	500	79.0	121	2	US-08-483-636-64	Sequence 64, Appl
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19	499.5	78.9	120	5	PCT-US95-10053-29	Sequence 29, Appl
20	499.5	78.9	120	5	PCT-US96-09448-32	Sequence 32, Appl
21	499	78.8	108	1	US-08-436-463-15	Sequence 15, Appl
22	489.5	77.3	120	5	PCT-US95-10053-28	Sequence 28, Appl
23	489.5	77.3	120	5	PCT-US96-09448-31	Sequence 31, Appl
24	482	76.1	114	1	US-08-436-463-16	Sequence 16, Appl
25	470.5	74.3	126	4	US-09-225-322B-4	Sequence 4, Appl1
26	470.5	74.3	141	4	US-09-225-322B-2	Sequence 2, Appl1
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29	454	71.7	121	4	US-09-025-769B-37	Sequence 37, Appl
30	454	71.7	121	4	US-09-025-769B-61	Sequence 61, Appl
31	445	70.3	123	5	PCT-US95-10053-27	Sequence 27, Appl
32	445	70.3	123	5	PCT-US96-09448-30	Sequence 30, Appl
33	443	70.0	499	4	US-09-049-672A-1	Sequence 1, Appl
34	440.5	69.6	139	2	US-08-553-501A-59	Sequence 59, Appl
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36	437.5	69.1	139	2	US-08-553-501A-61	Sequence 61, Appl
37	437.5	69.1	139	2	US-09-205-231-61	Sequence 61, Appl
38	436	68.9	123	3	US-08-290-592E-30	Sequence 30, Appl
39	433.5	68.5	120	3	US-08-553-501A-90	Sequence 90, Appl
40	433.5	68.5	120	3	US-09-205-231-90	Sequence 90, Appl
41	431.5	68.2	141	2	US-08-345-321-10	Sequence 10, Appl
42	430.5	68.0	120	2	US-08-553-501A-91	Sequence 91, Appl
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RESULT 1
US-08-483-636-4
Sequence 4, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corp./Corporate
Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
TELEPHONE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-483-636-4

Query Match

Best Local Similarity 90.1%; Score 569; DB 2; Length 140;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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DB 80 YNPSLKSRLLTSKDTSSNOVFELKITSVDFTATYTCARRVSLTAYAMDYWGOSTSVTS 139
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DB 140 S 140

RESULT 2

Sequence 4, Application US/08483632
Patent No. 5928904

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5090
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-483-632-4

Query Match 89.9%; Score 569; DB 2; Length 140;
Best Local Similarity 90.1%; Pred. No. 4.6e-50;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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DB 20 QVTLKESGPGILQPSQTLSTLTCSPGFSLSSTGSGVSWIRQPSGKLEMLAHYWDKKR 79
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QY 121 S 121
DB 140 S 140

RESULT 3

Sequence 10, Application US/08483636
Patent No. 5914110

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5090
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-483-636-10

Query Match 89.9%; Score 569; DB 2; Length 141;
Best Local Similarity 90.1%; Pred. No. 4.7e-50;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;QY 1 QVTLKESGPGILQPSQTLSTLTCSPGFSLSSTGSGVSWIRQPSGKLEMLAHYWDKKR 60
DB 20 QVTLKESGPGILQPSQTLSTLTCSPGFSLSSTGSGVSWIRQPSGKLEMLAHYWDKKR 79
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QY 121 S 121
DB 140 S 140

Db 21 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHITYWDDKR 80
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QY 121 S 121
Db 141 S 141

RESULT 4
US-08-483-632-10

; Sequence 10, Application US/08483632

; Patent No. 5928904

; GENERAL INFORMATION:

; APPLICANT: Holmes, Stephen D.

; APPLICANT: Gross, Mitchell S.

; APPLICANT: Sylvester, Daniel R.

; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: SmithKline Beecham Corp./Corporate

; ADDRESSEE: Intellectual Property

; STREET: P.O. Box 1539 / UW2220

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,632

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/117366

; FILING DATE: 07-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/136783

; FILING DATE: 14-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US/94/10308

; FILING DATE: 07-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 270-5024

; TELEFAX: (215) 270-5090

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 141 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-483-632-10

Query Match 89.9%; Score 569; DB 2; Length 141;

Best Local Similarity 90.1%; Pred. No. 4.7e-50;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHITYWDDKR 60
Db 21 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHITYWDDKR 80
QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYAMDYWGQGTSTVVS 120
Db 81 YNPISLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYAMDYWGQGTSTVVS 140
QY 121 S 121
Db 141 S 141

Db 81 YNPISLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYAMDYWGQGTSTVVS 140
QY 121 S 121
Db 141 S 141

RESULT 5
US-08-197-834-7

; Sequence 7, Application US/08197834

; Patent No. 5639455

; GENERAL INFORMATION:

; APPLICANT: SHIMAMURA, TOSHIRO

; APPLICANT: NAKAZAWA, HARUMI

; APPLICANT: HAMURO, JUNJI

; TITLE OF INVENTION: IMMUNOSUPPRESSANT

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/197,834

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 028173/1993

; FILING DATE: 17-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5639455man F.

; REGISTRATION NUMBER: 24,618

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 246 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-197-834-7

Query Match 89.7%; Score 567.5; DB 1; Length 246;

Best Local Similarity 89.6%; Pred. No. 1.3e-49;

Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHITYWDDKR 60
Db 123 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHITYWDDKR 182
QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYAMDYWGQGTSTVVS 116
Db 183 YNPISLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYAMDYWGQGTSTVVS 241
QY 117 VTVSS 121
Db 242 VTVSS 246

RESULT 6
US-08-436-463-14
; Sequence 14, Application US/08436463

Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-14

Query Match 87.1%; Score 551.5; DB 1; Length 122;
Best Local Similarity 91.4%; Pred. No. 2.2e-48;
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Db 1 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIROPSCGKLEMLAHYWDKDR 60
8 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIROPSCGKLEMLAHYWDKDR 67

QY 61 YNPFLKRLTISKDTSSNOVFLKITSVDTSDTATYCCARRSLTAVAMDYGOSTS 116
DB 68 YNPFLKRLTISKDTSSNOVFLKITSVDTSDTATYCCARRSLTAVAMDYGOSTS 122

RESULT 7
PCT-US95-07372-10
Sequence 10 Application PC/TUS9507372
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research Foundation
TITLE OF INVENTION: Calcium Binding Recombinant
TITLE OF INVENTION: Antibody Against Protein C
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07372
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF106CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: HPC-4 Heavy Chain Variable Region (YH Gamma)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 20..139
OTHER INFORMATION: /note="Gln" at position 20 starts
OTHER INFORMATION: mature peptide."

PCT-US95-07372-10

Query Match 82.5%; Score 522.5; DB 5; Length 139;
Best Local Similarity 84.3%; Pred. No. 2.1e-45;
Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIROPSCGKLEMLAHYWDKDR 60
DB 20 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIROPSCGKLEMLAHYWDKDR 79

QY 61 YNPFLKRLTISKDTSSNOVFLKITSVDTSDTATYCCARRSLTAVAMDYGOSTSVTS 120
DB 80 YNPFLKRLTISKDTSSNOVFLKITSVDTSDTATYCCARRSLTAVAMDYGOSTSVTS 138

QY 121 S 121
DB 139 S 139

RESULT 8
US-08-553-501a-88
Sequence 88 Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SAITO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-553-501A-88

Query Match 82.4%; Score 521.5; DB 2; Length 120;
Best Local Similarity 83.7%; Pred. No. 2.2e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

OY 1 QVTLKESGPGILQSPQTLSTLCFSFGSLSTSGMGVSWIRPSPGKGLMLAHYWDKDR 60
DB 1 QVTLKESGPGILQSPQTLSTLCFSFGSLSTSGMGVSWIRPSPGKGLMLAHYWDKDR 60
OY 61 YNPISLKSRLTISKDPSNQVFLKITSVDRTATAYYCARVSLFAY--AMDYWGQGSTVT 118
DB 61 YNPALKGRLLTISKDPSNQVFLKITSVDRTATAYYCARVSLFAY--AMDYWGQGSTVT 117
OY 119 VSS 121
DB 118 VSS 120

RESULT 9

US-09-205-231-88

Sequence 88, Application US/09205231

Patent No. 6121423

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/205,231

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-205-231-88

Query Match 82.4%; Score 521.5; DB 3; Length 120;
Best Local Similarity 83.7%; Pred. No. 2.2e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

OY 1 QVTLKESGPGILQSPQTLSTLCFSFGSLSTSGMGVSWIRPSPGKGLMLAHYWDKDR 60
DB 1 QVTLKESGPGILQSPQTLSTLCFSFGSLSTSGMGVSWIRPSPGKGLMLAHYWDKDR 60
OY 61 YNPISLKSRLTISKDPSNQVFLKITSVDRTATAYYCARVSLFAY--AMDYWGQGSTVT 118
DB 61 YNPALKGRLLTISKDPSNQVFLKITSVDRTATAYYCARVSLFAY--AMDYWGQGSTVT 117
OY 119 VSS 121
DB 118 VSS 120

RESULT 10

US-08-553-501A-29

Sequence 29, Application US/08553501A

Patent No. 5856135

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,501A

FILING DATE: 20-FEB-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP94/00859

FILING DATE: 30-MAY-1994

CURRENT APPLICATION DATA:

APPLICATION NUMBER: JP 5-129787

FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-501A-29

Query Match 82.4%; Score 521.5; DB 2; Length 139;
Best Local Similarity 83.7%; Pred. No. 2,7e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

1 QVTLKESGPIILPSPQTLSTLCSFSGFSLSTSGMGVSWINOPSGKLEMLAHIMYDDKR 60
20 QVTLKESGPIILPSPQTLSTLCSFSGFSLSTSGMGVSWINOPSGKLEMLAHIMYDDKR 79
61 YNPSLKSRLTISKDTSSNQVFLKITSVDRDTATYYCARRVSLTAY--ANDYMGQGTSTVT 118
80 YNPALKGRLLTISKDTSSNQVFLKITSVDRDTATYYCARRVSLTAY--MEDYDEAMDYMGQGTSTVT 136

OY 119 VSS 121
DB 137 VSS 139

RESULT 11

US-09-205-231-29
Sequence 29, Application US/09205231
Patent No. 6121423
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-205-231-29

Query Match 82.4%; Score 521.5; DB 3; Length 139;
Best Local Similarity 83.7%; Pred. No. 2,7e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

1 QVTLKESGPIILPSPQTLSTLCSFSGFSLSTSGMGVSWINOPSGKLEMLAHIMYDDKR 60
20 QVTLKESGPIILPSPQTLSTLCSFSGFSLSTSGMGVSWINOPSGKLEMLAHIMYDDKR 79
61 YNPSLKSRLTISKDTSSNQVFLKITSVDRDTATYYCARRVSLTAY--ANDYMGQGTSTVT 118
80 YNPALKGRLLTISKDTSSNQVFLKITSVDRDTATYYCARRVSLTAY--MEDYDEAMDYMGQGTSTVT 136

OY 119 VSS 121
DB 137 VSS 139

RESULT 12

US-08-290-592E-32
Sequence 32, Application US/08290592E
Patent No. 5824307
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
ADDRESSEE: OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,592E
FILING DATE: August 15, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-290-592E-32

Query Match 80.0%; Score 506.5; DB 2; Length 120;

Best Local Similarity 81.8%; Pred. No. 7.2e-44;
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Oy 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSNIRPSPGKLEMLAHYWDGDKR 60
Db 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSNIRPSPGKLEMLAHYWDGDKR 60
Oy 61 YNPFLKSRLLTSKRTSSNOVFLKITSVDTRATATYTCARRVSLRAYAMDYNGOGTSVTVS 120
Db 61 YNPFLKSRLLTSKRTSSNOVFLKITSVDTRATATYTCARRVSLRAYAMDYNGOGTSVTVS 119

Oy 121 S 121
Db 120 S 120

RESULT 13
US-08-436-463-2
Sequence 2, Application US/08436463
Patent No. 5760185

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoaki
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTI-BODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: KIMACHI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 143 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-463-2

Query Match 79.9%; Score 505.5; DB 1; Length 143;
Best Local Similarity 79.8%; Pred. No. 1.1e-43;
Matches 99; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

Oy 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSNIRPSPGKLEMLAHYWDGDKR 60
Db 20 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSNIRPSPGKLEMLAHYWDGDKR 79

Oy 61 YNPFLKSRLLTSKRTSSNOVFLKITSVDTRATATYTCARRVSLRAYAMDYNGOGTSV 117
Db 80 YNPFLKSRLLTSKRTSSNOVFLKITSVDTRATATYTCARRVSLRAYAMDYNGOGTSV 139

Oy 118 TVSS 121
Db 140 TVSA 143

RESULT 14
US-08-436-463-17

Sequence 17, Application US/08436463
Patent No. 5760185

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoaki
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTI-BODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: KIMACHI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-463-17

Query Match 79.6%; Score 504; DB 1; Length 108;
Best Local Similarity 90.8%; Pred. No. 1.1e-43;
Matches 99; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

Oy 9 PGIQPSQTLSTLCFSFGSLSTSGMGVSNIRPSPGKLEMLAHYWDGDKRYPFLSKR 68
Db 1 PGIQPSQTLSTLCFSFGSLSTSGMGVSNIRPSPGKLEMLAHYWDGDKRYPFLSKR 59
Oy 69 LTISKRTSSNOVFLKITSVDTRATATYTCARRVSLRAYAMDYNGOGTS 116
Db 60 LTISKRTSSNOVFLKITSVDTRATATYTCARRVSLRAYAMDYNGOGTS 108

RESULT 15
US-08-483-636-12

Sequence 12, Application US/08483636
Patent No. 5914110

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.

XX 07-SEP-1993; 930S-0117366.
 PR 14-OCT-1993; 930S-0136783.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX WPI: 1995-123387/16.
 DR N-PSDB; AAQ83491.
 XX
 PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
 from high affinity mabs - useful in treatment of IL-4-mediated
 PT and IGE-mediated allergic conditions
 PS Disclosure; Fig.2; 97pp; English.
 XX
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 clone 3B9 was positive. CDNA clones of the 3B9 light and heavy
 chains were cloned into pGEM7f and transformed into E. coli
 DH5-alpha. The clones were sequenced (AAQ83490-91), and used for
 CC antibody engineering.
 CC
 SQ Sequence 140 AA:
 Query Match 89.9%; Score 569; DB 16; Length 140;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPQILPQSQTLSITCSFSGFSLSSTSGMGVSWIRPGSGKLEMLAHYWD DDKR 60
 DB 20 QVTLKESGPQILPQSQTLSITCSFSGFSLSSTSGMGVSWIRPGSGKLEMLAHYWD DDKR 79
 QY 61 YNPSLKSRLITISKDTSSNOVFELKITSDVDFDTATYTCARVSLTAYAMDYMGGTSYTVS 120
 DB 80 YNPSLKSRLITISKDTSSNOVFELKITSDVDFDTATYTCARVSLTAYAMDYMGGTSYTVS 139
 QY 121 S 121
 DB 140 S 140
 RESULT 2
 AA123768
 ID AAY23768 standard; Protein; 140 AA.
 XX
 C AAY23768;
 DT 13-SEP-1999 (first entry)
 DE Heavy chain variable region of murine IL-4 antibody 3B9.
 XX
 DE Heavy chain variable region of murine IL-4 antibody 3B9.
 XX
 KW chimeric antibody: humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.
 XX
 OS Mus sp.
 XX
 PN US5928904-A.
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 950S-0483632.
 XX
 PR 07-JUN-1995; 950S-0483632.
 PR 07-SEP-1993; 930S-0117366.
 PR 14-OCT-1993; 930S-0136783.
 PR 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 XX WPI: 1999-429500/36.
 DR N-PSDB; AAX85885.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for
 treating IL4-mediated conditions
 PS Example 3; Fig 2; 50pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.
 CC The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 CC
 SQ Sequence 140 AA:
 Query Match 89.9%; Score 569; DB 20; Length 140;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPQILPQSQTLSITCSFSGFSLSSTSGMGVSWIRPGSGKLEMLAHYWD DDKR 60
 DB 20 QVTLKESGPQILPQSQTLSITCSFSGFSLSSTSGMGVSWIRPGSGKLEMLAHYWD DDKR 79
 QY 61 YNPSLKSRLITISKDTSSNOVFELKITSDVDFDTATYTCARVSLTAYAMDYMGGTSYTVS 120
 DB 80 YNPSLKSRLITISKDTSSNOVFELKITSDVDFDTATYTCARVSLTAYAMDYMGGTSYTVS 139
 QY 121 S 121
 DB 140 S 140
 RESULT 3
 AA18121
 ID AAY18121 standard; Protein; 140 AA.
 XX
 AC AAY18121;
 DT 11-AUG-1999 (first entry)
 DE Heavy chain sequence for murine 3B9 antibody.
 XX
 DE Heavy chain sequence for murine 3B9 antibody.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Mus sp.
 XX
 PN US5914110-A.
 PD 22-JUN-1999.
 XX
 PF 07-JUN-1995; 950S-0483636.
 XX
 PR 07-JUN-1995; 950S-0483636.
 PR 07-SEP-1993; 930S-0117366.
 PR 14-OCT-1993; 930S-0136783.
 PR 07-SEP-1994; 94WO-US10308.

PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI: 1999-370482/31.
 DR N-PSDB; AAY79520.
 XX
 PT Recombinant IL4 antibodies
 XX
 PS Claim 24; Fig 2; 50pp; English.
 XX
 CC This sequence represents the heavy chain of the murine 3B9
 CC antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 XX
 SQ Sequence 140 AA;
 XX
 Query Match 89.9%; Score 569; DB 20; Length 140;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 XX
 QY 1 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDKKR 60
 DB 20 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDKKR 79
 XX
 QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYGCARRVSLRAYAMDVGQSTSYVS 120
 DB 80 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYGCARRVSLRAYAMDVGQSTSYVS 139
 XX
 QY 121 S 121
 DB 140 S 140
 XX
 RESULT 4
 AAR70191
 ID AAR70191 standard; Protein; 141 AA.
 XX
 AC AAR70191;
 XX
 DE 20-SEP-1995 (first entry)
 XX
 DE Chimeric antibody 3B9 heavy chain.
 XX
 KM Chimeric antibody; antibody engineering; monoclonal antibody;
 KM MAb; interleukin-4; IL-4; allergy.
 XX
 OS Homo sapiens; Mus sp.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..19
 FT /label= sig-peptide
 FT 51..57
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT 72..87
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT 120..130
 FT /label= CDR
 FT /note= "complementarity determining region"
 XX
 FT Peptide
 XX
 FT
 XX
 PN WO9507301-A.
 XX
 PD 16-MAR-1995.
 XX

PF 07-SEP-1994; 94WO-US10308.
 XX
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI: 1995-123387/16.
 DR N-PSDB; AAQ83492.
 XX
 CC Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 CC from high affinity mAbs - useful in treatment of IL-4-mediated
 CC and IgE-mediated allergic conditions
 XX
 PS Disclosure; Fig.3; 97pp; English.
 XX
 CC A human/mouse chimeric antibody heavy chain variable region was
 CC constructed (given in AAR70191) that contained the mouse anti-human
 CC IL-4 Mab 3B9 variable region including 3 CDRs (AAR70198-200) and a
 CC human antibody signal peptide (AAR70193). The construct was used
 CC for humanized antibody production.
 XX
 SQ Sequence 141 AA;
 XX
 Query Match 89.9%; Score 569; DB 16; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 XX
 QY 1 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDKKR 60
 DB 21 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDKKR 80
 XX
 QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYGCARRVSLRAYAMDVGQSTSYVS 120
 DB 81 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYGCARRVSLRAYAMDVGQSTSYVS 140
 XX
 QY 121 S 121
 DB 141 S 141
 XX
 RESULT 5
 AAY23769
 ID AAY23769 standard; Protein; 141 AA.
 XX
 AC AAY23769;
 XX
 DE 13-SEP-1999 (first entry)
 XX
 DE Heavy chain variable region of murine/human chimeric antibody 3B9.
 XX
 KM Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KM chimeric antibody; humanised antibody; IL-4-mediated allergic reaction;
 KM immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KM conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KM rheumatoid arthritis; host-versus-graft disease; renal disease;
 KM allergy.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN US5928904-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-0483632.
 XX
 PR 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvestre DR;
 XX
 DR WPI: 1999-429500/36.
 DR N-PSDB; AAX85886.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 XX
 PS Example 3; Fig 3; 50pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic
 CC and pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 CC
 SQ Sequence 141 AA;

Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPILOPQSOTLSITCSFGSFLSTSGMGVSWIRPGSGKLEMLAHYWDKKR 60
 DB 21 QVTLKESGPILOPQSOTLSITCSFGSFLSTSGMGVSWIRPGSGKLEMLAHYWDKKR 80
 QY 61 YNPSLSRLTISKDTSSNOVFLKITSVDPRATYYCARRVSLTAYAMDYGOGTSVTS 120
 DB 81 YNPSLSRLTISKDTSSNOVFLKITSVDPRATYYCARRVSLTAYAMDYGOGTSVTS 140
 QY 121 S 121
 DB 141 S 141

RESULT 6
 AAY18125
 AAY18125 standard; Protein; 141 AA.

XX AAY18125;
 DT 11-AUG-1999 (first entry)
 XX
 DE Chimeric 3B9 monoclonal antibody heavy chain.
 XX
 KW Antibody; Interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PF 07-JUN-1995; 9505-0483636.
 XX
 PR 07-JUN-1995; 9505-0483636.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.

XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvestre DR;
 XX
 DR WPI: 1999-370482/31.
 DR N-PSDB; AAX79542.
 XX
 PT Recombinant IL4 antibodies
 XX
 PS Example 5; Fig 3; 50pp; English.
 XX
 CC This sequence represents the light chain of the chimeric
 CC 3B9 antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 CC
 SQ Sequence 141 AA;

Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPILOPQSOTLSITCSFGSFLSTSGMGVSWIRPGSGKLEMLAHYWDKKR 60
 DB 21 QVTLKESGPILOPQSOTLSITCSFGSFLSTSGMGVSWIRPGSGKLEMLAHYWDKKR 80
 QY 61 YNPSLSRLTISKDTSSNOVFLKITSVDPRATYYCARRVSLTAYAMDYGOGTSVTS 120
 DB 81 YNPSLSRLTISKDTSSNOVFLKITSVDPRATYYCARRVSLTAYAMDYGOGTSVTS 140
 QY 121 S 121
 DB 141 S 141

RESULT 7
 AAR58612
 AAR58612 standard; Protein; 246 AA.

XX AAR58612;
 DT 28-APR-1995 (first entry)
 XX
 DE IL-6 binding inhibitor.
 XX
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP617126-A.
 XX
 PD 28-SEP-1994.
 XX
 PF 16-FEB-1994; 94EP-0102346.
 XX
 PR 17-FEB-1993; 93JP-0028173.
 XX
 PA (AJIN) AJINOKOTO KK.
 XX
 PI Hamuro J, Nakazawa H, Shimamura T;
 XX
 DR WPI: 1994-295777/37.
 DR N-PSDB; AAO70612.
 XX
 PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to

PT Its receptor - useful for treating auto-immune disease induced
 or aggravated by IL-6
 PS Claim 5; Page 18; 26pp; English.
 XX AAQ70612 codes for human interleukin-6 binding inhibitor, the
 CC polypeptide described in AAR58612. This polypeptide inhibits the
 CC binding of human IL-6 to its receptor, and can therefore be
 CC useful in the treatment of a variety of autoimmune diseases;
 CC specifically in the treatment of rheumatoid arthritis, septic
 CC shock due to bacterial infection and multiple myeloma.
 XX
 SQ Sequence 246 AA;

Query Match 89.7%; Score 567.5; DB 15; Length 246;
 Best Local Similarity 89.6%; Pred. No. 4.4e-48;
 Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKLEMLAHYWD DDKR 60
 |||
 123 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKLEMLAHYWD DDKH 182
 |||
 QY 61 YNP SLKSR LITSKDTSSNQVFLKITSVDTRDTATYTCARRVSLA---YANDYWGQGTG 116
 |||
 DB 183 YNP SLKSR LITSKDTSSNQVFLKITSVDTRDTATYTCARRVSLA---YANDYWGQGTG 241
 |||
 QY 117 VTSS 121
 |||
 DB 242 VTSS 246

RESULT 8

AAR54101 standard; Protein: 122 AA.

AA54101;

08-FEB-1995 (first entry)

Humanised MAb H-chain.

XX Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIM.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX

Key Location/Qualifiers
 Region 31..37
 Region /Label- CDR1
 Region 52..67
 Region /Label- CDR2
 Region 100..111
 Region /Label- CDR3

JP06141885-A.

24-MAY-1994.

05-NOV-1992; 92JP-0322476.

05-NOV-1992; 92JP-0322476.

(KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

WPI: 1994-205040/25.

N-PSDB: AAO68709.

Recombinant anti-HIV monoclonal antibody - capable of
 neutralising strains which can not be neutralised by anti-IIIB
 and IIIM antibodies
 Disclosure: Page 13; 23pp; Japanese.

XX The sequences given in AAR54101-02 represent the heavy and light chains
 CC respectively of the humanised monoclonal antibody (MAb) of the
 CC invention. The antibody has the ability to neutralise human
 CC immunodeficiency virus. The antibody is classified as IgG kappa and
 CC has the sequence RIGPGR or RVGPGR in the principal neutralising
 CC domain. The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIM strains.
 XX
 SQ Sequence 122 AA;

Query Match 86.3%; Score 546.5; DB 15; Length 122;
 Best Local Similarity 87.7%; Pred. No. 2.3e-46;
 Matches 107; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKLEMLAHYWD DDKR 60
 |||
 DB 1 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKLEMLAHYWD DDKH 60
 |||
 QY 61 YNP SLKSR LITSKDTSSNQVFLKITSVDTRDTATYTCARRVSL-TAYANDYWGQGTG 119
 |||
 DB 61 YNP SLKSR LITSEDTSSNQVFLKITSVDTRDTATYTCARRVYFNGSDFMHMGQGTG 120
 |||
 QY 120 SS 121
 |||
 DB 121 SS 122

RESULT 9

AAR88109 standard; peptide: 120 AA.

AAR88109;

25-JUL-1996 (first entry)

Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.

XX Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour.
 XX

OS Mus musculus.

PN W09534652-A1.

21-DEC-1995.

09-JUN-1995; 95WO-US07372.

10-JUN-1994; 94US-0259321.

(OKLA-) OKLAHOMA MED RES FOUND.

Esmon CT, Rezaie A;

WPI: 1996-049681/05.

N-PSDB: AAT09300.

Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by
 PT thrombin-thrombomodulin, e.g. for treating tumours
 XX
 PS Claim 2; Page 29; 41pp; English.

This is the amino acid sequence of the mature peptide from the murine
 CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.
 CC HPC-4 recognises the activation peptide region (AAR88106) of the heavy
 CC chain of protein C, a vitamin K-dependent plasma protein zymogen.
 CC Protein C is converted to activated protein C (APC) by cleavage between
 CC the Arg-Leu amino acid contained within the activation peptide sequence.
 CC HPC-4 prevents protein C activation to APC by binding to this region.

CC The DNA sequences encoding the variable regions of the heavy and light
 CC chains of the antibody (AA09299-302) were used to construct humanised
 CC antibodies using the PCR primers AA09303-9. The humanised antibodies
 CC are useful as inhibitors of coagulation and can be used for the treatment
 CC of tumours by inhibiting the anticoagulant activity of APC by preventing
 CC conversion of protein C to APC.

XX Sequence 120 AA;

Query Match 82.5%; Score 522.5; DB 17; Length 120;
 Best Local Similarity 84.3%; Pred. No. 5.2e-44;
 Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTCSGFSLSSTSGMGVSWIRQPSGKLEMLAHIMWDDDKR 60
 DB 1 QVTLKESGPGILQPSQTLSTCSGFSLSSTSGMGVSWIRQPSGKLEMLAHIMWDDDKR 60

QY 61 YNPSLKSRLLTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGOSTSVTVS 120
 DB 61 YNPSLKSRLLTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGOSTSVTVS 119

QY 121 S 121
 DB 120 S 120

RESULT 10
 AAR8107 standard; Protein: 139 AA.

AC AAR8107;

DT 25-JUL-1996 (first entry)

DE Murine anti-Protein C MAb HPC-4 VH gamma protein.

XX Epitope; activation: heavy chain; protein C; vitamin K; plasma protein;

KW zymogen; cleavage; mouse; humanised antibody; variable region;

KM light chain; inhibition; anticoagulant; coagulation; tumour.

OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..19 /note= "signal peptide"

FT Peptide 20..139 /note= "mature peptide"

XX MO9534652-A1.

XX 21-DEC-1995.

XX 09-JUN-1995; 95MO-US07372.

XX 10-JUN-1994; 94US-0259321.

XX (OKLA-) OKLAHOMA MED RES FOUND.

XX Esmon CT, Rezaie A;

XX WPI: 1995-049681/05.

XX N-PSDB: AA09299.

XX Calcium-binding monoclonal antibody immunoreactive with Protein C

XX inhibits Protein C anticoagulant activation by

XX thrombin-thrombomodulin, e.g. for treating tumours

XX Claim 2; Page 29; 41pp; English.

CC to activated protein C (APC) by cleavage between the Arg-Leu amino acid
 CC contained within the activation peptide sequence. HPC-4 prevents
 CC protein C activation to APC by binding to this region. The DNA sequences
 CC encoding the variable regions of the heavy and light chains of the
 CC antibody (AA09299-302) were used to construct humanised antibodies using
 CC the PCR primers AA09303-9. The humanised antibodies are useful as
 CC inhibitors of coagulation and can be used for the treatment of tumours by
 CC inhibiting the anticoagulant activity of APC by preventing conversion of
 CC protein C to APC.

XX Sequence 139 AA;

Query Match 82.5%; Score 522.5; DB 17; Length 139;
 Best Local Similarity 84.3%; Pred. No. 6.1e-44;
 Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTCSGFSLSSTSGMGVSWIRQPSGKLEMLAHIMWDDDKR 60
 DB 20 QVTLKESGPGILQPSQTLSTCSGFSLSSTSGMGVSWIRQPSGKLEMLAHIMWDDDKR 79

QY 61 YNPSLKSRLLTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGOSTSVTVS 120
 DB 80 YNPSLKSRLLTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGOSTSVTVS 138

QY 121 S 121
 DB 139 S 139

RESULT 11
 AAR67655 standard; Protein: 139 AA.

AC AAR67655;

DT 21-AUG-1995 (first entry)

DE Mouse heavy chain variable region amino acid sequence.

XX Primer; PCR; amplification; kappa; light chain; variable region; mouse; human;

KW interleukin; antibody; hypodermis; CDR; framework; constant region;

KM heavy chain; disorder; antigenicity.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19 /label= signal peptide

FT Peptide 20..139 /label= mature peptide

XX WO9428159-A.

XX 08-DEC-1994.

XX 30-MAY-1994; 94MO-JP00859.

XX 31-MAY-1993; 93JP-0129787.

XX (CHUS) CHUGAI SEIYAKU KK.

XX (CHUS) CHUGAI PHARM CO LTD.

XX Hirata Y, Sato K, Tsuchiya M;

XX WPI: 1995-022828/03.

XX N-PSDB: AA075889.

XX Antibody against IL-6 - useful for the therapy and treatment of

XX IL-6 related disorders.

XX Claim 10; Page 49; 82pp; Japanese.

XX The deduced amino acid sequence of the heavy chain variable region of

CC the mouse anti-human interleukin-6 (IL-6) antibody. The gene was
CC amplified by primers (AA075876-87) from cDNA derived from mRNA from
CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19
CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to
CC generate constructs (see AA075914-7) encoding fragments of an antibody to
CC the human IL-6 comprising (a) a light chain with (1) a variable region
CC containing 3 complementarity determining regions (CDR) (AA07201-3)
CC inserted into several framework regions (FR) (AA07204-7) and (11) a human
CC light chain constant region and (b) a heavy chain with (1) a variable
CC region containing 3 CDR (AA07212-4) inserted into an FR (AA07215-8) and
CC (11) a human light chain constant region. The FR of the light chain may
CC be mouse derived (AA075888) or from the human antibody FR1. The heavy
CC chain FR may also be mouse derived (AA075889) or from the human antibody
CC DAW. The antibodies are used in the treatment of IL-6 related
CC disorders. The antibodies are useful as they have low antigenicity due to
CC the use of human derived sequences and low antigenicity mouse derived
CC sequences.

SO Sequence 139 AA:

Query Match

Best Local Similarity 82.4%; Score 521.5; DB 16; Length 139;

Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLCSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDKDK 60
DB 20 QVTLKESGPGILQPSQTLSTLCSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDKDK 79
QY 61 RYNPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAY--AMDYWGQTSVT 118
DB 80 RYNPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAY--AMDYWGQTSVT 136
QY 119 VSS 121
DB 137 VSS 139

RESULT 12

ABG67188

ID ABG67188 standard; Protein; 121 AA.

AC ABG67188;

DT 24-SEP-2002 (first entry)

DE Human IgG1 antibody heavy chain variable region 15H4VH.

KW Hepatitis C virus vaccine; HCV; hypervariable region 1; HVRI;

KW envelope protein E2; antibody; helper T-lymphocyte; IgG1;

KW cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.

OS Homo sapiens.

PN WO200245743-A2.

PD 13-JUN-2002.

PE 07-DEC-2001; 2001WO-GB05421.

PR 09-DEC-2000; 2000GB-0030102.

PR 18-DEC-2000; 2000GB-0030789.

PA (ALLA) ALLAIN J.

PI Allain J, Li C, Piccolella E;

PS WPI: 2002-508540/54.

PT Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T
PT lymphocytes and/or cytotoxic T lymphocytes able to bind to the
PT hypervariable 1 region of the infecting HCV strain
PS Example 4; Fig 2; 52pp; English.

XX The present invention relates to a hepatitis C virus (HCV) vaccine
CC comprising different groups of peptides each group being capable of
CC raising, in an infected individual, an antibody able to bind to the
CC hypervariable 1 (HVRI) region of the envelope protein E2 of the
CC infecting HCV strain. The different groups of peptides are
CC administered sequentially to raise antibodies, helper T-lymphocytes,
CC and cytotoxic T-lymphocytes which are cross-reactive to the HVRI
CC region of the infecting HCV. The vaccines are useful for preventing
CC and treating chronic HCV infections. ABG67186-ABG67189 represent
CC variable regions of human IgG1 antibody heavy chain.

SO Sequence 121 AA:

Query Match

Best Local Similarity 82.1%; Score 520; DB 23; Length 121;

Matches 104; Conservative 7; Mismatches 7; Indels 4; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLSTLCSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDKDK 59
DB 1 QVTLKESGPGILQPSQTLSTLCSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDKDK 60
QY 60 RYNPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAYAMDYWGQTSVT 119
DB 61 RYNPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAYAMDYWGQTSVT 117
QY 120 SS 121
DB 118 SS 119

RESULT 13

AAZ25396

ID AAZ25396 standard; Protein; 121 AA.

AC AAZ25396;

DT 07-SEP-1999 (first entry)

DE WO9932630 Seq ID 35.

KW Paraquat; antibody; light chain; herbicide; resistant; crop plant;

KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;

KW free radical; lipid peroxidation; electron transport; photosystem II;

KW vacuole; cell surface; cytotoxic; sensitive.

OS Undefined.

PN WO9932630-A1.

PD 01-JUL-1999.

PE 15-DEC-1998; 98WO-GB03760.

PR 19-DEC-1997; 97GB-0026955.

PA (ZENE) ZENECA LTD.

PI Holt DC, Jones PG;

PS WPI: 1999-405173/34.

Herbicide binding proteins and related polynucleotides

Disclosure; Page 43-44; 60pp; English.

This invention describes a novel herbicide binding protein which can
confer herbicide resistance activity. Crop plants, such as soybean,
cotton, tobacco, sugarcane, oilseed rape, canola, flax, sunflower,
potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,
barley, oat, turf grass, forage grass, sugar cane, pea, field bean,
rice, pine, poplar, apple, grape, citrus or nut plants, transformed
with a herbicide binding protein gene are resistant to the herbicide.

CC Hence, weeds can be selectively controlled in a field of the transformed
CC crops. The plants are substantially resistant or tolerant to herbicides,
CC such as paraquat or diquat, that inhibit photosynthesis by accepting
CC electrons from photosystem II thus generating free radicals which cause
CC lipid peroxidation or by blocking electron transport in photosystem II.
CC The herbicide binding proteins advantageously sequester the herbicide,
CC e.g. at the cell surface or in the vacuoles of a treated plant.
CC Sequestration at the cell surface prevents the entry of the herbicide
CC into the cell so that the herbicide cannot reach its intracellular target
CC and exert any significant cytotoxic effect. The herbicide binding protein
CC inhibits the mobility of the herbicide from the application site to the
CC whole plant preventing the herbicide reaching particularly sensitive
CC organs. Additionally, tolerant plants can be produced against herbicides
CC that have more than one target site.

SQ Sequence 121 AA;

Query Match	81.58;	Score 516;	DB 20;	Length 121;
Best Local Similarity	81.88;	Pred. NO. 2.3e-43;		
Matches 99; Conservative	7;	Mismatches 15;	Indels 0;	Gaps 0;

db 1 EVKLQESGPILQPSQTLSLTCSFSGFSLTTSGMGVTWIRQPSGKGLEWLTIDYWDDGKD 60

Oy 61 YNLSLKSRLTISKDTSSNOVFLKITSVDPTDATTATYCCARRSLTAYAMDYGQGTSTVTS 120
||||| : ||||| | : |||||
Dd 61 YNSLKSRLTISKDTSKNQVFLQLASVDSADTATATYCTRFYSGKSTAMDSMGQGVSTVS 120

QY	121 S 121
Db	121 S 121

RESULT 14
AAB09778
ID AAB09778 standard; Protein; 259 AA

DT 06-SEP-2000 (first entry)

DE Antiviral scFv-antibody against a component of the TMV replicase.

KW molecular pathogenicide; plant disease; resistance; antibody; scFv;

deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.

Tobacco mosaic virus.

PN WO200023593-A2.

PD 27-APR-2000

PF 15-OCT-1999; 99WO-EP07844.

PR 16-OCT-1998; 98EP-0119630.

XX

XX

PI Spiegel H, Zimmerman S, Emans N, Holzem A;

DR WPI; 2000-339692/29.

PT New fusion proteins and gene constructs for expressing agents (antibodies, enzymes, vectors or molecular pathogenicides), useful for PT protecting plants against pathogens and increasing resistance to PT disease -

PS Example 6; Flg 23b; 193pp; English.

XX The present invention describes a fusion protein (I) comprising at least
CC one binding domain specifically recognising an epitope of a plant
CC pathogen and at least one further domain comprising a protein or peptide
CC sequence which is toxic to the pathogen or detrimental to its
CC replication, transmission or life cycle. Also described is a
CC pathogenicide (II) comprising (I) and a cellular targeting sequence
CC and/or membrane localisation sequence and/or motif that leads to
CC membrane anchoring; or at least one binding domain that specifically
CC recognises a viral movement and/or replicase protein. The fusion
CC protein, pathogenicide, polynucleotide, vectors, and compositions from
CC the present invention are useful for the protection of a plant against
CC the action of a pathogen. The kit from the present invention is useful
CC for carrying out the methods and may be employed in different
CC applications, for example in the diagnostic field or as research tools.
CC The kit or its components, such as the fusion protein, pathogenicide,
CC polynucleotides, vectors or compositions are useful in plant cell and
CC plant tissue culture, in agriculture. They are extremely useful for
CC breeding new varieties of plants that display improved properties such as
CC resistance to pathogens. AAA55587 to AAA56702 and AAB09774 to B097820
CC represent sequences used in the exemplification of the present
XX invention.

Sequence 259 AA:

Sequence 259 AA;

Query Match	81.5%;	Score 516;	DB 21;	Length 259;
Best Local Similarity	81.8%;	Pred. No. 5.6e-43;		
Matches 99;	Conservative 7;	Mismatches 15;	Indels 0;	Gaps 0;

```
QY 1 QVTLKESGPILQPSQTLSTLCFSFGSFLSTSGMGVSWIRQPSGKGLEMLAHYWDDDR 60
      |||||:|||||:|||||:|||||:|||||
DB 3 QVTLKESGPILKPSQTLSTLCFSFGSFLSTSGMGVSWIRQPSGKGLEMLAHYWDDDR 62
```

63 YNPLSRQLISKDTRNQVFLRITNVDATATYICARGYYGNDSPFAYMGOGTLLTVS 122

RESULT 15

ID AAB70885

AC AAB70885;

DT 12-JUL-2001 (first entry)

DE TMV 54K protein derived monoclonal antibody scFv54-1.

KW Monoclonal antibody; detection; diagnosis; infection; scFv54-1.

OS Tobacco mosaic virus.

PN EP1092769-A2.

PD 18-APR-2001.

PF 18-AUG-2000; 2000EP-0117845.

PR 15-OCT-1999; 99DE-1049855.

XX

XX

PI Schillerberg S;

DR WPI; 2001-267745/28.

PT New polypeptide tag, useful for detection and isolation of fusion

PR proteins, is derived from tobacco mosaic virus 54k protein and reacts
PR specifically with antibodies

PS Example 1; Page 7-8; 12pp; German.

XX This invention describes a novel polypeptide with tag sequence (I) or a
CC sequence derived from (I) by replacement of one or more amino acids (aa),
CC provided the three-dimensional/tertiary structure remains essentially
CC unchanged. The invention also describes (1) expression vector encoding a
CC fusion protein (FP) of a target polypeptide (II) and (I); (2) FP encoded
CC by the vector of (1); (3) antibodies (Ab), or their fragments, directed
CC against (I); and (4) kit containing the vector of (1) and optionally Ab.
CC (I) are used for isolation and/or detection of fusion polypeptides that
CC contain (I), by reaction with (I)-specific antibodies (Ab). Ab are used
CC for isolation, purification and/or detection of polypeptides (also for
CC determination of molecular weight, cell localization, post-translational
CC modification and interaction with other factors), and for diagnosis of
CC infection by tobacco mosaic virus (TMV). (I) is recognized by very
CC specific, high-affinity antibodies that do not cross-react significantly
CC with other cellular proteins (bacterial or eukaryotic). This sequence
CC represents the monoclonal antibody scFv54-1 which is used to illustrate
CC the method of the invention.

XX Sequence 259 AA:

Query Match 81.5%; Score 516; DB 22; Length 259;

Best Local Similarity 81.8%; Pred. No. 5.6e-43;

Matches 99; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

OY	1	QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIRQPSGKLEMLAHYWD	60
DB	3	QVTLKESGPGILKPSQTLSTLCFSFGSLSTSGMGVSWIRQPSGKLEMLAHYWD	62
OY	61	YNPSLKSRLTISKDTSSNQVFLKITSVDTRATYVCARVSLTAYAMDYWGQGT	120
DB	63	YNPSLKSRLTISKDTSSNQVFLKITSVDTRATYVCARVSLTAYAMDYWGQGT	122
OY	121	S 121	
DB	123	S 123	

Search completed: July 9, 2003, 12:40:02
Job time : 71 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:40:08 ; Search time 22 Seconds

(without alignments)
640.309 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSTL.....SLFAYANDYMGQGSYTVSS 121

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PC1_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/PC1US_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEM_PUB pep:*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_NEM_PUB pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	121	9	US-09-759-112a-7
2	569	89.9	140	9	US-09-879-461-4
3	569	89.9	141	9	US-09-879-461-10
4	555	87.7	123	9	US-09-995-529-12
5	506.5	80.0	120	10	US-09-158-120A-32
6	506.5	80.0	143	10	US-09-881-823-8
7	502	79.3	141	9	US-09-879-461-12
8	499.5	78.9	120	9	US-10-011-931-3
9	470.5	74.3	126	9	US-10-265-713-4
10	470.5	74.3	126	10	US-09-764-304-4
11	470.5	74.3	141	9	US-10-265-713-2
12	470.5	74.3	141	10	US-09-764-304-2
13	468.5	74.0	120	9	US-09-771-415-2
14	468.5	74.0	120	10	US-09-796-848A-4
15	468.5	74.0	450	9	US-09-996-265-208
16	468.5	74.0	450	9	US-09-996-265-208
17	467.5	73.9	120	10	US-09-158-120A-31
18	466.5	73.7	120	9	US-09-771-415-18
19	466.5	73.7	120	9	US-09-771-415-20

20	466.5	73.7	120	9	US-09-771-415-24	Sequence 24, Appl
21	466.5	73.7	120	9	US-09-771-415-26	Sequence 26, Appl
22	466.5	73.7	450	9	US-09-996-268-210	Sequence 210, App
23	466.5	73.7	450	9	US-09-996-268-240	Sequence 240, App
24	466.5	73.7	450	9	US-09-996-265-210	Sequence 210, App
25	466.5	73.7	450	9	US-09-996-265-240	Sequence 240, App
26	465.5	73.5	450	9	US-09-996-288-238	Sequence 238, App
27	465.5	73.5	450	9	US-09-996-288-242	Sequence 242, App
28	465.5	73.5	450	9	US-09-996-288-244	Sequence 244, App
29	465.5	73.5	450	9	US-09-996-288-246	Sequence 246, App
30	465.5	73.5	450	9	US-09-996-265-238	Sequence 238, App
31	465.5	73.5	450	9	US-09-996-265-242	Sequence 242, App
32	465.5	73.5	450	9	US-09-996-265-244	Sequence 244, App
33	465.5	73.5	450	9	US-09-996-265-246	Sequence 246, App
34	464.5	73.4	120	9	US-09-771-415-22	Sequence 22, Appl
35	463.5	73.2	450	9	US-09-996-268-232	Sequence 232, App
36	463.5	73.2	450	9	US-09-996-268-234	Sequence 234, App
37	462.5	73.1	120	9	US-09-996-268-7	Sequence 7, Appl
38	462.5	73.1	120	9	US-09-996-265-7	Sequence 7, Appl
39	462.5	73.1	120	10	US-09-796-848A-2	Sequence 2, Appl
40	462.5	73.1	450	9	US-10-135-636-1	Sequence 1, Appl
41	461.5	72.9	450	9	US-09-996-268-232	Sequence 232, App
42	461.5	72.9	450	9	US-09-996-268-234	Sequence 234, App
43	461.5	72.9	450	9	US-09-996-268-236	Sequence 236, App
44	461.5	72.9	450	9	US-09-996-265-232	Sequence 232, App
45	461.5	72.9	450	9	US-09-996-265-234	Sequence 234, App

ALIGNMENTS

RESULT 1
US-09-759-112a-7
; Sequence 7, Application US/09759112a
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LI
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOYPIC ANTIBODY REACTI
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-09-759-112a-7

Query Match 100.0%; Score 633; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMKVSMIRPSCGKGLMLAHYWDCKR 60
|||||
DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMKVSMIRPSCGKGLMLAHYWDCKR 60
|||||
QY 61 YNPSLKSRLTISKDPSNQVFLKITSVYTRPTATYCARRSYLAAYANDYMGQGSYTVSS 120
|||||
DB 61 YNPSLKSRLTISKDPSNQVFLKITSVYTRPTATYCARRSYLAAYANDYMGQGSYTVSS 120
|||||
QY 121 S 121
|
DB 121 S 121
|

RESULT 2
US-09-879-461-4
; Sequence 4, Application US/09879461
; Publication No. US20020193575A1

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-879-461-4

Query Match 89.9%; Score 569; DB 9; Length 140;
Best Local Similarity 90.1%; Pred. No. 6.1e-43;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 1 QVTLKESGPGIILPQSQTLSITCSFSGFSLSTSGMGVSWIRPSGKGLEMLAHITYWDDKR 60
|||||
QY 61 YNPSLSRLTISDTSNOVFLKITSVDFTATYYCARVSLTAYAMDYWGCGTSVTYS 120
|||||
Db 80 YNPSLSRLTISDTSNOVFLKITSVDFTATYYCARRETVFYWFYWGAGTIVTVS 139
|||||

QY 121 S 121
|
Db 140 S 140

RESULT 3
US-09-879-461-10
Sequence 10, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-879-461-10

Query Match 89.9%; Score 569; DB 9; Length 141;
Best Local Similarity 90.1%; Pred. No. 6.1e-43;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 1 QVTLKESGPGIILPQSQTLSITCSFSGFSLSTSGMGVSWIRPSGKGLEMLAHITYWDDKR 60
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QY 21 QVTLKESGPGIILPQSQTLSITCSFSGFSLSTSGMGVSWIRPSGKGLEMLAHITYWDDKR 80
|||||
Db 61 YNPSLSRLTISDTSNOVFLKITSVDFTATYYCARVSLTAYAMDYWGCGTSVTYS 120
|||||
QY 81 YNPSLSRLTISDTSNOVFLKITSVDFTATYYCARRETVFYWFYWGAGTIVTVS 140
|||||

QY 121 S 121
|
Db 141 S 141

RESULT 4
US-09-995-529-12
Sequence 12, Application US/09995529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 123
TYPE: PRT

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutcon, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-879-461-12

Query Match 79.3% Score 502; DB 9; Length 141;
Best Local Similarity 76.9% Pred. No. 4.7e-37;
Matches 93; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVTLKESGPILOPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
DB 21 QVTLKESGPILOPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 80
QY 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTA-YANDYWGCGTSVTV 120
DB 81 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTA-YANDYWGCGTSVTV 140
QY 121 S 121
DB 141 S 141

RESULT 8

US-10-011-931-3

Sequence 3, Application US/10011931.
Publication No. US20030026806A1

GENERAL INFORMATION:

APPLICANT: WITTE, ALISON
APPLICANT: VARNUM, BRIAN C.
APPLICANT: OZAN, ZUEMING
APPLICANT: VEZINA, CHRIS
TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
FILE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
CURRENT FILING DATE: 2002-04-01
PRIORITY APPLICATION NUMBER: US 60/244,118
PRIORITY FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Version 3.1
SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-10-011-931-3

Query Match 78.9% Score 499.5; DB 9; Length 120;
Best Local Similarity 81.0% Pred. No. 6.6e-37;
Matches 98; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
DB 1 QVTLKESGPILOPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
QY 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTA-YANDYWGCGTSVTV 120
DB 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTA-YANDYWGCGTSVTV 119
QY 121 S 121
DB 120 S 120

RESULT 9

US-10-265-713-4

Sequence 4, Application US/10265713
Publication No. US20030095964A1

GENERAL INFORMATION:

APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KURAMA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIORITY APPLICATION NUMBER: US/09/225,322
PRIORITY FILING DATE: 1999-01-05/08/454,680
PRIORITY APPLICATION NUMBER: US 08/408,133
PRIORITY FILING DATE: 1995-05-31
PRIORITY APPLICATION NUMBER: US 08/292,178
PRIORITY FILING DATE: 1995-03-21
PRIORITY APPLICATION NUMBER: JP 3-238375
PRIORITY FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 126
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-265-713-4

Query Match 74.3% Score 470.5; DB 9; Length 126;
Best Local Similarity 75.4% Pred. No. 2.4e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
DB 5 QVTLKESGPILOPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 64
QY 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTA-YANDYWGCGTSVTV 119
DB 65 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTA-YANDYWGCGTSVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 10

US-09-764-304-4

Sequence 4, Application US/09764304
Patent No. US20020026036A1

GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO

APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 126
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Rat hybridoma
US-09-764-304-4

Query Match 74.3%; Score 470.5; DB 10; Length 126;
Best Local Similarity 75.4%; Pred. No. 2,4e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLSTLCSFGFSSTSGMGVSWIRPSGKGLEWLAHIYDDDKR 60
|||||
5 QVTLKESGPGILQPSQTLSTLCSFGFSSTSGMGVSWIRPSGKGLEWLAHIYDDDKR 64
|||||
QY 61 YNPSLKSRLTTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YAMDWGQGSTVTV 119
|||||
DB 65 YNPSLKNRLTTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YAMDWGQGSTVTV 124
|||||
QY 120 SS 121
||
DB 125 SS 126

RESULT 11

US-10-265-713-2
Sequence 2, Application US/10265713
Publication No. US20030095964A1

GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 141
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-265-713-2

Query Match 74.3%; Score 470.5; DB 9; Length 141;
Best Local Similarity 75.4%; Pred. No. 2.7e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFGFSSTSGMGVSWIRPSGKGLEWLAHIYDDDKR 60
|||||
DB 20 QVTLKESGPGILQPSQTLSTLCSFGFSSTSGMGVSWIRPSGKGLEWLAHIYDDDKR 79
|||||
QY 61 YNPSLKSRLTTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YAMDWGQGSTVTV 119
|||||
DB 80 YNPSLKNRLTTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YAMDWGQGSTVTV 139
|||||
QY 120 SS 121
||
DB 140 SS 141

RESULT 12

US-09-764-304-2
Sequence 2, Application US/09764304
Patent No. US20020026036A1

GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 141
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Rat hybridoma
US-09-764-304-2

Query Match 74.3%; Score 470.5; DB 10; Length 141;
Best Local Similarity 75.4%; Pred. No. 2.7e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFGFSSTSGMGVSWIRPSGKGLEWLAHIYDDDKR 60
|||||
DB 20 QVTLKESGPGILQPSQTLSTLCSFGFSSTSGMGVSWIRPSGKGLEWLAHIYDDDKR 79
|||||
QY 61 YNPSLKSRLTTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YAMDWGQGSTVTV 119
|||||
DB 80 YNPSLKNRLTTSKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YAMDWGQGSTVTV 139
|||||

OY 120 SS 121
DB 140 SS 141

RESULT 13

US-09-771-415-2
Sequence 2, Application US/09771415
Patent No. US20020164326A1
GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Koenig, Scott
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: ultra high affinity Neutralizing Antibodies
FILE REFERENCE: 469201-520
CURRENT APPLICATION NUMBER: US/09/771,415
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mouse human
OTHER INFORMATION: chimeric antibody heavy chain variable chain
US-09-771-415-2

Query Match 74.0%; Score 468.5; DB 9; Length 120;
Best Local Similarity 72.7%; Pred. No. 3.5e-34;
Matches 88; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

OY 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
DB 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
OY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYWGOSTSVTS 120
DB 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYWGOSTSVTS 120
OY 121 S 121
DB 120 S 120

RESULT 14

US-09-796-848A-4
Sequence 4, Application US/09796848A
Patent No. US20020098189A1
GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
Producing Them
FILE REFERENCE: 469201-526
CURRENT APPLICATION NUMBER: US/09/796,848A
CURRENT FILING DATE: 2001-10-30
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 120
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain
OTHER INFORMATION: variable region sequence of a humanized antibody.
US-09-796-848A-4

Query Match 74.0%; Score 468.5; DB 10; Length 120;
Best Local Similarity 72.7%; Pred. No. 3.5e-34;
Matches 88; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

OY 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
DB 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
OY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYWGOSTSVTS 120
DB 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYWGOSTSVTS 120
OY 121 S 121
DB 120 S 120

RESULT 15

US-09-996-288-208
Sequence 208, Application US/09996288
Patent No. US20020177126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophyl
and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 208
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-208

Query Match 74.0%; Score 468.5; DB 9; Length 450;
Best Local Similarity 72.7%; Pred. No. 1.4e-33;
Matches 88; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

OY 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
DB 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
OY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYWGOSTSVTS 120
DB 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYWGOSTSVTS 120
OY 121 S 121
DB 120 S 120

Search completed: July 9, 2003, 12:43:48
Job time: 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:37:27 ; Search time 39 Seconds

(without alignments)
298.263 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSTL.....SLRAYANDYWGQSTVTVSS 121Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551.5	87.1	122	2 S11740	Ig heavy chain pre
2	543.5	85.9	143	2 PT0174	Ig heavy chain pre
3	491	77.6	107	2 A49442	Ig heavy chain V r
4	474.5	75.0	113	2 S26465	Ig heavy chain V r
5	472.5	74.6	116	2 S26328	Ig heavy chain V r
6	471	74.4	138	2 S31513	Ig heavy chain - h
7	460	72.7	121	2 S09959	Ig heavy chain V r
8	454.5	71.8	124	2 A49002	Ig heavy chain V r
9	448	70.8	103	2 B25913	Ig heavy chain pre
10	436	68.9	374	2 S69339	Ig heavy chain V r
11	419.5	66.3	120	2 GIHUCO	Ig heavy chain V-I
12	412	65.1	121	2 A36005	Ig heavy chain V r
13	410	64.8	119	2 S18555	Ig heavy chain V r
14	407	64.3	125	1 MHHMWC	Ig heavy chain V-I
15	402.5	63.6	147	1 G2HUCS	Ig heavy chain pre
16	395	62.4	121	2 GIHUCB	Ig heavy chain V-I
17	390.5	61.7	122	2 S20809	Ig heavy chain V r
18	384.5	60.7	120	2 PL0087	Ig heavy chain V r
19	384	60.7	144	1 G2MS14	Ig heavy chain V r
20	383.5	60.6	118	2 S18556	Ig heavy chain pre
21	382	60.3	146	2 S09711	Ig heavy chain V r
22	379.5	60.0	117	2 S38563	Ig heavy chain V r
23	377	59.6	96	2 S26924	Ig heavy chain V r
24	377	59.6	140	2 I37822	Ig variable region
25	376	59.4	147	2 S13519	Ig heavy chain V r
26	373.5	59.0	122	2 A49049	Ig heavy chain V r
27	373.5	59.0	137	2 S31676	Ig heavy chain V r
28	372	58.8	135	2 S31511	Ig heavy chain - h
29	371	58.6	96	2 S26923	Ig heavy chain V r

30	371	58.6	109	2 PH1023	Ig heavy chain V r
31	371	58.6	119	1 GIHUCW	Ig heavy chain V-I
32	371	58.6	140	2 S55028	Ig heavy chain V r
33	370.5	58.5	130	2 S30534	Ig heavy chain V r
34	370	58.5	155	2 S31512	Ig heavy chain - h
35	369	58.3	130	2 S31690	Ig heavy chain V r
36	368.5	58.2	139	2 A32456	Ig heavy chain pre
37	368.5	58.2	141	2 S52446	Ig heavy chain V r
38	368	58.1	117	2 I57810	gene C72-3A1 prote
39	366	57.8	111	2 S26324	Ig heavy chain V r
40	363	57.3	149	2 S30752	Ig heavy chain pre
41	362	57.2	128	2 S31514	Ig heavy chain - h
42	360.5	57.0	129	2 S44114	Ig heavy chain V r
43	360	56.9	127	2 S19668	Ig heavy chain V r
44	360	56.9	135	2 S78051	Ig heavy chain pre
45	359.5	56.8	139	2 S31586	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S11740

Ig heavy chain precursor V-D-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S11740

R:Hayakawa, K.; Carmack, C.E.; Hyman, R.; Hardy, R.R.

A:Submitted to the EMBL Data Library, May 1990

A:Description: Natural autoantibodies to thymocytes. Origin, VH genes, fine specific

A:Reference number: S11740

A:Accession: S11740

A:Molecule type: mRNA

A:Residues: 1-122 <EMBL>

A:Cross-references: EMBL:X53097; NID:952368; PIDN:CA37261.1; PID:6762983

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:22-106/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 87.1%; Score 551.5; DB 2; Length 122;
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy

1 QVTLKESGPGILQPSQTLSTLSCFSGFSLSGSGVSIROPSGKLEMLAHYVDDDKR 60

8 QVTLKESGPGILQPSQTLSTLSCFSGFSLSGSGVSIROPSGKLEMLAHYVDDDKR 67

Qy 61 YNPSIKSRLTISKDTSNOVFLKITSVDTRDPATYVCARRVSLRAYANDYWGQST 116

Db 68 YNPSIKSRLTISKDTSNOVFLKITSVDTRDPATYVCARRVSLRAYANDYWGQST 122

RESULT 2

PT0174

Ig heavy chain precursor V region (IdB5.7) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C:Accession: PT0174

R:Perlelli, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.

A:Title: Specificity and variable region cDNA sequence of an isogenetic monoclonal ant

A:Reference number: PT0174; MUID:91287738; PMID:1712074

A:Accession: PT0174

A:Molecule type: mRNA

A:Residues: 1-143 <PER>

A:Experimental source: strain BALB/c

C:Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:34-118/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.9%; Score 543.5; DB 2; Length 143;
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

S09959

Ig heavy chain V region (31-9D) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999

C:Accession: S09959

R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies

A:Reference number: S09959; MID:90269328; PMID:2347362

A:Accession: S09959

A:Molecule type: mRNA

A:Residues: 1-121 <RE>

A:Cross-references: EMBL:X51847; NID:955247; PIDN:CA36140.1; PID:9930215

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-99/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 72.7%; Score 460; DB 2; Length 121;

Matches 90; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

RESULT 9

B25913

Ig heavy chain precursor V region (BFL23) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996

C:Accession: B25913

R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987

A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region gen

A:Reference number: A94148; MID:87175692; PMID:3104915

A:Accession: B25913

A:Molecule type: DNA

A:Residues: 1-103 <LA>

A:Note: the authors translated the codon TGT for residue 11 as Ser

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:19-103/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 70.8%; Score 448; DB 2; Length 103;

Matches 85; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 60

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

OY 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWDKKR 64

RESULT 11

G1HUCO

Ig heavy chain V-II region (Cor) - human (tentative sequence)

C:Species: Homo sapiens (man)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 31-Mar-2000

C:Accession: A02089

R:Press, E.M.; Hogg, N.M.

Biochem. J. 117, 641-660, 1970

A:Title: The amino acid sequences of the Fd fragments of two human gamma1 heavy chains.

A:Reference number: A90250; MUID:70258837; PMID:5449120

A:Accession: A02089

A:Molecule type: protein

A:Residues: 1-120 <PRE>

C:Comment: This chain was isolated from an IgG1 myeloma protein.

C:Genetics:

A:Gene: GDB:IGHV

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; Immunoglobulin; pyroglytamic acid

F:15-96/Domain: Immunoglobulin homology <IMM>

F:22-94/Disulfide bonds: #status experimental

F:62/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match

Best Local Similarity 66.3%; Score 419.5; DB 1; Length 120;

Matches 84; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

G1HUCO

Ig heavy chain V-II region (Cor) - human (tentative sequence)

C:Species: Homo sapiens (man)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 31-Mar-2000

C:Accession: A02089

R:Press, E.M.; Hogg, N.M.

Biochem. J. 117, 641-660, 1970

A:Title: The amino acid sequences of the Fd fragments of two human gamma1 heavy chains.

A:Reference number: A90250; MUID:70258837; PMID:5449120

A:Accession: A02089

A:Molecule type: protein

A:Residues: 1-120 <PRE>

C:Comment: This chain was isolated from an IgG1 myeloma protein.

C:Genetics:

A:Gene: GDB:IGHV

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; Immunoglobulin; pyroglytamic acid

F:15-96/Domain: Immunoglobulin homology <IMM>

F:22-94/Disulfide bonds: #status experimental

F:62/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match

Best Local Similarity 64.8%; Score 410; DB 2; Length 119;

Matches 75; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60

Db 1 QVTLKESGPILOPQSLTSCFSFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60


```

OY      61 YNPSLRSLTISKDTSNQVFLKITSVPTRDPAFYCAR----RVSLEAYANDYWGQGS 116
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 YSPSLRSRLTGTGKDTSKNQVLLTITNMDPVDSGYFCARPPWRPTGNLGGFDXWGQSTL 120
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      117 VTSS 121
          |||||
DB      121 VTSS 125
          |||||

```

RESULT 15

G2HUCS

Ig heavy chain precursor V-II region (Cess) - human

C:Species: Homo sapiens (man)

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 02-Sep-1997

C:Accession: A02090

R:Takahashi, N.; Noma, T.; Honjo, T.

Proc. Natl. Acad. Sci. U.S.A. 81, 5194-5198, 1984

A:Title: Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that del

Reference number: A02090; MUID:84298107; PMID:6089186

Accession: A02090

R:Molecule type: mRNA

A:Residues: 1-147 <TAK>

A:Note: the sequence was determined from the differentiated gene

as Ser. and CAG for residue 147 as Ser

C:Gene: GDB:IGHV

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

A:Introns: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-147/Product: Ig heavy chain V-II region (Cess) #status predicted <MAT>

F:34-118/Region: V segment

F:119-132/Domain: immunoglobulin homology <IMM>

F:133-147/Region: D segment

Query Match 63.6%; Score 402.5; DB 1; Length 147;

Best Local Similarity 62.3%; Pred. No. 5.1e-31;

Matches 76; Conservative 16; Mismatches 23; Indels 7; Gaps 1;

```

OY      1 QVTAKESGPGILQPSQTLSTCSFSGSLSTSGWGVSWIRQPSGKLEMLAHITWDGDKR 60
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      20 QVNLRESGPAVKATHTLTCTFSGSLVNTRGMSVSWIRQPPGKALEMLARIDWDGDKY 79
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
          61 YNPSLRSLTISKDTSNQVFLKITSVPTRDPAFYCA-----RVSLEAYANDYWGQ 113
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      80 YGTSLERTLTISKDTSKNQVLLKTYNMDPADTAITYCARMOVYTWREVWITSNAPDIWGQ 139
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      114 GT 115
          ||
DB      140 GT 141
          ||

```

Search completed: July 9, 2003, 12:42:45

Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:24:47 ; Search time 23 Seconds

218.202 Million cell updates/sec

Title: US-09-759-112A-7

Sequence: 1 QVTLKESGPIIQPSQTLSL.....SLTAYAMDYWGQGTSTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419.5	66.3	120	HV2B_HUMAN	P01815 homo sapien
2	407	64.3	125	HV2D_HUMAN	P01817 homo sapien
3	402.5	63.6	147	HV2H_HUMAN	P04438 homo sapien
4	395	62.4	121	HV2E_HUMAN	P01818 homo sapien
5	384	60.7	144	HV43_MOUSE	P01819 mus musculus
6	371	58.6	119	HV2C_HUMAN	P01816 homo sapien
7	358.5	56.6	126	HV2J_HUMAN	P01814 homo sapien
8	353	55.8	127	HV46_MOUSE	P01822 mus musculus
9	327	51.7	115	HV44_MOUSE	P01820 mus musculus
10	317	50.1	129	HV2E_XETLA	P01824 homo sapien
11	315.5	49.8	135	HV02_XETLA	P20957 xenopus laevis
12	312.5	49.4	116	HV60_MOUSE	P1851 mus musculus
13	309.5	48.9	146	HV2I_HUMAN	P06311 homo sapien
14	306.5	48.4	126	HV3K_HUMAN	P01772 homo sapien
15	305	48.2	117	HV2G_HUMAN	P01825 homo sapien
16	302	47.7	121	HV3J_HUMAN	P01771 homo sapien
17	299.5	47.3	116	HV61_MOUSE	P18532 mus musculus
18	299.5	47.3	122	HV3G_HUMAN	P01768 homo sapien
19	299.5	47.3	136	HV16_MOUSE	P01782 mus musculus
20	298	47.1	113	HV47_MOUSE	P01823 mus musculus
21	293	46.3	116	HV45_MOUSE	P01821 mus musculus
22	288	45.5	117	HV62_MOUSE	P18533 mus musculus
23	287.5	45.4	122	HV3H_HUMAN	P01769 homo sapien
24	287	45.0	136	HV01_XETLA	P20956 xenopus laevis
25	278.5	44.0	119	HV40_MOUSE	P01810 mus musculus
26	278	43.9	119	HV3I_HUMAN	P01770 homo sapien
27	275.5	43.5	119	HV37_MOUSE	P01807 mus musculus
28	273	43.1	117	HV41_MOUSE	P01811 mus musculus
29	272.5	43.0	119	HV38_MOUSE	P01808 mus musculus
30	271.5	42.9	116	HV3T_HUMAN	P01781 homo sapien
31	271	42.8	117	HV42_MOUSE	P01812 mus musculus
32	266	41.5	119	HV3L_HUMAN	P01773 homo sapien
33	262.5	41.5	114	HV3B_HUMAN	P01763 homo sapien

34	262.5	41.5	119	1	HV3N_HUMAN
35	261	41.2	115	1	HV3D_HUMAN
36	261	41.2	115	1	HV3E_HUMAN
37	260.5	41.2	118	1	HV3V_HUMAN
38	259.5	41.0	122	1	HV20_MOUSE
39	256.5	40.5	119	1	HV3N_HUMAN
40	256	40.4	118	1	HV39_MOUSE
41	256	40.4	123	1	HV24_MOUSE
42	256	40.4	142	1	HV01_RAT
43	255	40.3	123	1	HV23_MOUSE
44	255	40.3	123	1	HV25_MOUSE
45	254.5	40.2	115	1	HV3S_HUMAN
46	254.5	40.2	115	1	HV3S_HUMAN
47	254.5	40.2	115	1	HV3S_HUMAN
48	254.5	40.2	115	1	HV3S_HUMAN
49	254.5	40.2	115	1	HV3S_HUMAN
50	254.5	40.2	115	1	HV3S_HUMAN
51	254.5	40.2	115	1	HV3S_HUMAN
52	254.5	40.2	115	1	HV3S_HUMAN
53	254.5	40.2	115	1	HV3S_HUMAN
54	254.5	40.2	115	1	HV3S_HUMAN
55	254.5	40.2	115	1	HV3S_HUMAN
56	254.5	40.2	115	1	HV3S_HUMAN
57	254.5	40.2	115	1	HV3S_HUMAN
58	254.5	40.2	115	1	HV3S_HUMAN
59	254.5	40.2	115	1	HV3S_HUMAN
60	254.5	40.2	115	1	HV3S_HUMAN
61	254.5	40.2	115	1	HV3S_HUMAN
62	254.5	40.2	115	1	HV3S_HUMAN
63	254.5	40.2	115	1	HV3S_HUMAN
64	254.5	40.2	115	1	HV3S_HUMAN
65	254.5	40.2	115	1	HV3S_HUMAN
66	254.5	40.2	115	1	HV3S_HUMAN
67	254.5	40.2	115	1	HV3S_HUMAN
68	254.5	40.2	115	1	HV3S_HUMAN
69	254.5	40.2	115	1	HV3S_HUMAN
70	254.5	40.2	115	1	HV3S_HUMAN
71	254.5	40.2	115	1	HV3S_HUMAN
72	254.5	40.2	115	1	HV3S_HUMAN
73	254.5	40.2	115	1	HV3S_HUMAN
74	254.5	40.2	115	1	HV3S_HUMAN
75	254.5	40.2	115	1	HV3S_HUMAN
76	254.5	40.2	115	1	HV3S_HUMAN
77	254.5	40.2	115	1	HV3S_HUMAN
78	254.5	40.2	115	1	HV3S_HUMAN
79	254.5	40.2	115	1	HV3S_HUMAN
80	254.5	40.2	115	1	HV3S_HUMAN
81	254.5	40.2	115	1	HV3S_HUMAN
82	254.5	40.2	115	1	HV3S_HUMAN
83	254.5	40.2	115	1	HV3S_HUMAN
84	254.5	40.2	115	1	HV3S_HUMAN
85	254.5	40.2	115	1	HV3S_HUMAN
86	254.5	40.2	115	1	HV3S_HUMAN
87	254.5	40.2	115	1	HV3S_HUMAN
88	254.5	40.2	115	1	HV3S_HUMAN
89	254.5	40.2	115	1	HV3S_HUMAN
90	254.5	40.2	115	1	HV3S_HUMAN
91	254.5	40.2	115	1	HV3S_HUMAN
92	254.5	40.2	115	1	HV3S_HUMAN
93	254.5	40.2	115	1	HV3S_HUMAN
94	254.5	40.2	115	1	HV3S_HUMAN
95	254.5	40.2	115	1	HV3S_HUMAN
96	254.5	40.2	115	1	HV3S_HUMAN
97	254.5	40.2	115	1	HV3S_HUMAN
98	254.5	40.2	115	1	HV3S_HUMAN
99	254.5	40.2	115	1	HV3S_HUMAN
100	254.5	40.2	115	1	HV3S_HUMAN

ALIGNMENTS

Q0	SEQUENCE	120 AA;	13226 MW;	158A8529AE7EEB98 CRC64;
FT	CARBOHYD	62	62	N-LINKED (GLCNAC. . .).
FT	NON_TER	120	120	
FT	DISULFID	22	1	
FT	MOD_RES	1	1	PYRROLIDONE CARBOXYLIC ACID.
KW	Immunoglobulin V region;	Glycoprotein.		
DR	SMART; SMO0406; IgV; 1.			
DR	Pfam; PF00047; Ig; 1.			
DR	InterPro; IPR003596; IG_V.			
DR	InterPro; IPR003006; IG_MHC.			
DR	HSSP; P01825; 7EAB.			
CC	MISCLEIN.			
CC	-I- MYELOBLASTOSUS: THIS CHAIN WAS ISOLATED FROM AN IGCL MYELOMA PROTEIN.			
RT	heavy chain."			
RT	Biochem. J. 117:641-660(1970).			
RX	MEDLINE=70258837; PubMed=5449120;			
RA	Press E.M., Hogg N.M.;			
RN	"The amino acid sequences of the Fd fragments of two human gamma			
RN	SEQUENCE.			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxId=9606;			
ID	HY2B_HUMAN	STANDARD;	PRT;	120 AA.
IC	P01815:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	Ig heavy chain V-II region COR.			
OS	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
CC	NCBI_TaxId=9606;			
CC	SEQUENCE.			
RX	MEDLINE=70258837; PubMed=5449120;			
RA	Press E.M., Hogg N.M.;			
RT	"The amino acid sequences of the Fd fragments of two human gamma			
RT	heavy chain."			
RT	Biochem. J. 117:641-660(1970).			
CC	-I- MYELOBLASTOSUS: THIS CHAIN WAS ISOLATED FROM AN IGCL MYELOMA PROTEIN.			
DR	PIR; A02089; GIHUCO.			
DR	HSSP; P01825; 7EAB.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SMO0406; IgV; 1.			
KW	Immunoglobulin V region;	Glycoprotein.		
FT	MOD_RES	1	1	
FT	DISULFID	22	1	
FT	CARBOHYD	62	62	
FT	NON_TER	120	120	
Q0	SEQUENCE	120 AA;	13226 MW;	158A8529AE7EEB98 CRC64;

query match	66.38; Score 419.5; DB 1; Length 120;
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Matches	84;	Conservative	15;	Mismatches	19;	Indels	5;	Gaps	2.
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1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60

1 QVTLRESGPALVKPTQTLLTCTFSGFSLSTGMCVGWIRQPPGKGLEWLARIDWDDKY 60

61 YNPSLKSRLLISKDTSSNOVELKITSVDTTRDTATYYCARVSLTAYA--MDYWGQTSVT 118

61 YNTSLEIRLTISKDSRNQVL--TMDPVDATYYCARITVIPAPAGYMDVWGRTPT 117

119 VSS 121

118 VSS.120

V2D_HUMAN

C P01817;

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region MCE.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=8118242; PubMed=6780622;
RA Geber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
RA Litman G.W.;
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RT region of MCE."
RL J. Immunol. 126:1212-1216(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
CC CRYOIMMUNOGLOBULIN.
DR PIR: A02092; MHDMC.
DR HSSP: P01825; 7RAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 1 1
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47B55 CRC64;

Query Match 64.3%; Score 407; DB 1; Length 125;
Best Local Similarity 62.3%; Pred. No. 3e-34;
Matches 79; Conservative 17; Mismatches 25; Indels 4; Gaps 1;

QY 1 QVTLKESGPGIILPSQTLSTLCSPGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
DB 1 QVTLKESGPGIILPSQTLSTLCSPGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
QY 61 YNPSLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCAR---RVSILTAAMDYGQCTS 116
DB 61 YNPSLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCAR---RVSILTAAMDYGQCTS 116
QY 117 VTWSS 121
DB 117 VTWSS 125
DB 121 VTWSS 125

RESULT 3
HV2H_HUMAN STANDARD; PRT; 147 AA.
P04438;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region SESS precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298107; PubMed=6089186;
RA Takahashi N., Noma T., Honjo T.;
RT "Rearranged immunoglobulin heavy chain variable region (VH)
RT pseudogene that deletes the second complementarity-determining
RT region."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR PIR: A02090; G2HUCS.
DR HSSP: P01825; 7RAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
KW Immunoglobulin V region; Signal.

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FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.
FT DOMAIN 20 118 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16323 MW; FCBDCB3D00F6B666 CRC64;

Query Match 63.6%; Score 402.5; DB 1; Length 147;
Best Local Similarity 62.3%; Pred. No. 1e-33;
Matches 76; Conservative 16; Mismatches 23; Indels 7; Gaps 1;

QY 1 QVTLKESGPGIILPSQTLSTLCSPGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
DB 20 QVTLKESGPGIILPSQTLSTLCSPGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
QY 61 YNPSLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCA-----RVSILTAAMDYGQ 113
DB 80 YNPSLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCA-----RVSILTAAMDYGQ 113
QY 114 GT 115
DB 140 GT 141

RESULT 4
HV2H_HUMAN STANDARD; PRT; 121 AA.
P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains."
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR: A02093; G1HJHE.
DR HSSP: P01825; 7RAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 1 1
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 62.4%; Score 395; DB 1; Length 121;
Best Local Similarity 61.5%; Pred. No. 4.6e-33;
Matches 75; Conservative 20; Mismatches 25; Indels 2; Gaps 2;

QY 1 QVTLKESGPGIILPSQTLSTLCSPGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 59
DB 1 QVTLKESGPGIILPSQTLSTLCSPGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60
QY 60 RYNPSLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCARVSLTAAMDYGQCTSYV 119
DB 61 RYNPSLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCARVSLTAAMDYGQCTSYV 119
QY 120 SS 121
DB 120 SS 121
DB 121 SS 121

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RESULT 5
HY43_MOUSE STANDARD: PRT: 144 AA.
AC P01819;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki K., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes."
NL Nature 286:676-683(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IgG2B.
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CC EMBL: V00768; CAA24149.1;
DR PIR: A02094; G2MS14.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match
Best Local Similarity 60.7%; Score 384; DB 1; Length 144;
Matches 78; Conservative 17; Mismatches 23; Indels 10; Gaps 3;

1 QVTLKESGPGILPQSOTLSLTCSEFSGFSLSTSGMGVSMIRPGSGKLEMLAHYWDDDR 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
20 QVQLKESGPGILVAPQSLSITCTVSGFSL--TGYVNVNVRPGKGLMLGTIMNGSTD 77
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLAY-----ANDYWGQ 113
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
78 YNSTLKSRLTITKDNKSQVFLKMSLOTDTARYCA-SVSIYYGSRDKFTLDYWGQ 136
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
114 GTSVTSS 121
|||||
137 GTSVTSS 144

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RESULT 6
HY2C_HUMAN STANDARD: PRT: 119 AA.
AC P01816;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region DAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

RESULT 7
HY2A_HUMAN STANDARD: PRT: 126 AA.
AC P01814;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=7400511; PubMed=4742735;
RA Putnam F.W., Florent G., Paul C., Shinoda T., Shinazu A.;
RT "Complete amino acid sequence of the mu heavy chain of a human IgM
immunoglobulin."
NL Science 182:287-291(1973).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR: A02088; MH000U.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT DISULFID 22 97
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 14276 MW; AB50EBD0ABC296F CRC64;

Query Match
Best Local Similarity 56.6%; Score 358.5; DB 1; Length 126;
Matches 76; Conservative 19; Mismatches 26; Indels 5; Gaps 2;

1 QVTLKESGPGILPQSOTLSLTCSEFSGFSLSTSGMGVSMIRPGSGKLEMLAHYWD---D 57
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 QVTLKESGPGILVAPQSLSITCTVSGFSLSTSGMGVSMIRPGSGKLEMLA---WDIIND 57
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
58 DKRYNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLAYANDYWGQTSY 117
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
58 DKRYNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLAYANDYWGQTSY 115
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
116 TVSS 119

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QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLTSGMGVSMIRKPSGKLEWLAHYWDDKR 60
D 1 QVTLTEGSPALVVKPQGLTLTCTPFSGLSTSRMRVSMIRPPKALEWLAIBBDBKFY 60
QY 61 YNPSLKRRLTSKSDTSNOVFLKITSVDTDPATYCARV-SLTA----YANDYWGCGT 115
D 61 WSTSLRRLTSKSDTSNOVFLKITSVDTDPATYCARVSYMAGYVYVMDVWGCGT 120
QY 116 SVTVSS 121
D 121 TVTVSS 126

RESULT 8
HV46_MOUSE STANDARD; PRT: 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
gene segment."
RL Mol. Immunol. 26:431-434(1989).
RN [2]
RP MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
immunoglobulin heavy chain."
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN [3]
RP MEDLINE=79148756; PubMed=428562;
RA Schechter I., Wolf O., Zemel R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors."
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
chain of a mouse myeloma protein with anti-hapten activity."
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN [5]
RP MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RT "Unpublished results, cited by:
Polidan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
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or send an email to license@isb-sib.ch.)
CC -----
EMBL: M27638: AAA61337.1; -.
DR EMBL: X07880: CAA30727.1; -.

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DR PIR: P10102; AVMS35.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; signal.
FT SIGNAL 1
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 137 FRAMEWORK-4.
FT DISULFID 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
FT CONFLICT 15 15 G -> H (IN REF. 2).
FT CONFLICT 77 78 G -> YG (IN REF. 4).
FT CONFLICT 102 102 N -> D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 55.8%; Score 353; DB 1; Length 137;
Best Local Similarity 59.2%; Pred. No. 9e-29;
Matches 71; Conservative 19; Mismatches 28; Indels 2; Gaps 2;

QY 2 VTLKESGPGILQPSQTLSTLCSFSGFSLTSGMGVSMIRKPSGKLEWLAHYWDDKR 61
D 20 VQLESQGLVVKPQGLTLTCTPFSGLSTSRMRVSMIRPPKALEWLAIBBDBKFY 78
QY 62 NPSLKRRLTSKSDTSNOVFLKITSVDTDPATYCARVSLTA-YANDYWGCGTSVTVSS 121
D 79 NPSLKRRLTSKSDTSNOVFLKITSVDTDPATYCARVSLTA-YANDYWGCGTSVTVSS 137

RESULT 9
HV44_MOUSE STANDARD; PRT: 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region PJ14 precursor.
OS Mus musculus (mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch.)
CC -----
EMBL: V00767; CAA24148.1; -.
DR PIR: A02095; HVMS14.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.

```

KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19 IG HEAVY CHAIN V REGION PJ14.
 FT CHAIN 20 115
 FT NON_TER 115 115
 SO SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
 Query Match 51.7%; Score 327; DB 1; Length 115;
 Best Local Similarity 64.3%; Pred. No. 3,1e-26;
 Matches 63; Conservative 14; Mismatches 19; Indels 2; Gaps 1;
 QY 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSIKIPSGKGLMIAHYWDGDKR 60
 DB 20 QVQTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSIKIPSGKGLMIAHYWDGSTD 77
 QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAY-----AMDYWG 112
 DB 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAY-----AMDYWG 112
 QY 113 QGTSVTYSS 121
 DB 121 QGTVHWSS 129
 DB 121 QGTVHWSS 129
 RESULT 11
 HV02_XENLA STANDARD; PRT; 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 CC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=88176921; PubMed=2451244;
 RA Schwaeger J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced from cDNA sequence: implications for evolution of immunoglobulin domains".
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
 CC -----
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 CC -----
 CC EMBL: J03632; AAA49791.1; -
 DR PIR: B31933; B31933.
 DR HSSP: P01810; ZFB3.
 DR InterPro: IPR003506; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL 1 18
 FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
 FT NON_TER 135 135
 SO SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;
 Query Match 49.8%; Score 315.5; DB 1; Length 135;
 Best Local Similarity 52.1%; Pred. No. 5.3e-25;
 Matches 62; Conservative 20; Mismatches 34; Indels 3; Gaps 2;
 QY 3 TLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSIKIPSGKGLMIAHYWDGDKRYN 62
 DB 20 TLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSIKIPSGKGLMIAHYWDGDKRYN 77
 QY 63 PSLKSLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYAMDYWGQTSVTYSS 121
 DB 78 PSLKSLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYAMDYWGQTSVTYSS 135
 RESULT 12
 HV60_MOUSE
 ID HV60_MOUSE STANDARD; PRT; 116 AA.
 AC P18531;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region M315 precursor.
 OS Mus musculus (Mouse).
 CC Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=BAJB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response".
 RL J. Exp. Med. 169:2007-2019(1989).
 PIR: JT0509; HVMS31.


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Query Match          48.2% Score 305; DB 1; Length 117;  
Best Local Similarity 49.6%; Pred. No. 5.Le-24;  
Matches    60; Conservative   24; Mismatches 33; Indels    4; Gaps     2
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DY 1 QVTLKESGPGILAPSGQTLSLTCFSEGSFLSTSCMGVSNIROPSPKGLEMLHIYWDDKR 60
Db |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 1 QVOLESQSPGGIVRPSQTSLLTFCVSGSFNSND--YYTWVRPPGGGLGMIGCVFHGTSD 58

DY 61 YNPSLKSRLTISSKTSSNQOVFLKITSYTRDTATAYGCARVLTAAYADWQGCGTSYVS 120
Db |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 59 DTTPLRSRVTVMVPTSKMQGFSIRLSSVYAADTAITYCAR--NLINGCIDWMGQSLSYTVS 116

DY 121 S 121
Db |
 117 S 117

Search completed: July 9, 2003, 12:40:31
Job time : 23 secs

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Search completed: July  9, 2003, 12:40:31
Job time : 23 secs

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ID	HY2G_HUMAN	STANDARD;	PRT;	117 AA.
AC	P01825;			
CD	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
OS	Ig heavy chain V-II region NEMM.			
OC	Homo sapiens (Human).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE.			
RX	MEDLINE-77242302; PubMed-407927;			
RX	Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;			
RT	"Amino acid sequence of the VH region of a human myeloma			
RL	immunoglobulin (IgG New).";			
RN	Biochemistry 16:3412-3420(1977).			
SA	[2]			
SA	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.			
RX	MEDLINE-78066916; PubMed-618887;			
RT	Saul F.A., Amzel L.M., Poljak R.J.;			
RT	"Preliminary refinement and structural analysis of the Fab fragment			
RL	from human immunoglobulin new at 2.0-A resolution.";			
CC	J. Biol. Chem. 253:585-597(1978).			
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGg1 MYELOMA			
CC	PROTEIN.			
DR	PDB; A02100; G1HDM.			
DR	PDB; 7FAB; 31-JAN-94.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PFO0047; Ig; 1.			
DR	SMART; SM00406; IgV; 1.			
DR	Immunoglobulin V region; 3D-structure.			
FT	MOD_RES	1	1	PROLIDONE CARBOXYLIC ACID.
FT	STRAND	3	7	
FT	STRAND	11	12	
FT	TURN	14	15	
FT	STRAND	18	25	
FT	TURN	30	31	
FT	STRAND	33	39	
FT	TURN	41	42	
FT	STRAND	46	51	
FT	TURN	53	54	
FT	STRAND	57	59	
FT	HELIX	61	63	
FT	TURN	64	66	
FT	STRAND	67	72	
FT	TURN	73	76	
FT	STRAND	77	82	
FT	HELIX	87	89	
FT	STRAND	91	98	
FT	STRAND	104	107	
FT	STRAND	111	115	
FT	NON_TER	117	117	
Q	SEQUENCE	117 AA; 12790 MW; 2DA47B509562D237 CRC64;		

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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:34:22 ; Search time 79 Seconds
(Without alignments)
315.591 Million cell updates/sec

Title: US-09-759-112a-7
Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSL.....SLRAYADYWGQGTSTVYSS 121

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	471	74.4	121	4 Q9UL96	Q9UL96 homo sapien
2	398.5	63.0	121	11 Q99NG4	Q99NG4 mus musculu
3	370.5	58.5	482	11 Q91X92	Q91X92 mus musculu
4	361.5	57.1	496	4 Q96KX8	Q96KX8 homo sapien
5	361	57.0	119	4 Q9UL73	Q9UL73 homo sapien
6	356	56.2	97	4 Q43234	Q43234 homo sapien
7	354.5	56.0	613	4 Q96EY0	Q96EY0 homo sapien
8	343	54.2	479	11 Q99M22	Q99M22 mus musculu
9	341	53.9	588	4 Q8W0X4	Q8W0X4 mus sapien
10	341	53.9	597	4 Q9B0U0	Q9B0U0 homo sapien
11	341	53.9	618	4 Q96AA6	Q96AA6 homo sapien
12	338	53.4	597	4 Q9BOB8	Q9BOB8 homo sapien
13	337.5	53.3	150	4 Q95973	Q95973 homo sapien
14	331.5	52.4	122	4 Q9UL75	Q9UL75 homo sapien
15	305.5	48.3	147	4 Q9Y509	Q9Y509 homo sapien
16	302.5	47.8	613	4 Q8W0K1	Q8W0K1 homo sapien

17	301.5	47.6	473	4 Q8TC63	Q8TC63 homo sapien
18	295	46.6	113	4 Q9UL90	Q9UL90 homo sapien
19	288.5	45.6	112	4 Q9HCCL	Q9HCCL homo sapien
20	284.5	44.9	573	4 Q8W038	Q8W038 homo sapien
21	284	44.9	116	4 Q9UL93	Q9UL93 homo sapien
22	278.5	44.0	122	4 Q9UL84	Q9UL84 homo sapien
23	276.5	43.7	473	11 Q91Z05	Q91Z05 mus musculu
24	273.5	43.2	118	4 Q9UL91	Q9UL91 homo sapien
25	272.5	43.0	118	4 Q9UL72	Q9UL72 homo sapien
26	272	43.0	121	4 Q9UL71	Q9UL71 homo sapien
27	272	43.0	131	4 Q9UL88	Q9UL88 homo sapien
28	269.5	42.6	145	11 Q924Q9	Q924Q9 mus musculu
29	269.5	42.6	471	4 Q8TC77	Q8TC77 homo sapien
30	269.5	42.6	484	11 Q8VEA0	Q8VEA0 mus musculu
31	268.5	42.4	298	11 Q90YF0	Q90YF0 mus musculu
32	268.5	42.1	145	11 Q924P7	Q924P7 mus musculu
33	265.5	41.9	487	11 Q99KX4	Q99KX4 mus musculu
34	264	41.7	597	4 Q96BB9	Q96BB9 homo sapien
35	263	41.5	468	11 Q99LJ1	Q99LJ1 mus musculu
36	262.5	41.5	494	4 Q96K68	Q96K68 homo sapien
37	261.5	41.3	145	11 Q924R1	Q924R1 mus musculu
38	261.5	41.3	469	11 Q8R3V9	Q8R3V9 mus musculu
39	260.5	41.2	145	11 Q924Q6	Q924Q6 mus musculu
40	259.5	41.0	241	11 Q921A6	Q921A6 mus musculu
41	257	40.6	484	11 Q99LA6	Q99LA6 mus musculu
42	256	40.4	118	4 Q9UL74	Q9UL74 homo sapien
43	255.5	40.4	145	11 Q924R4	Q924R4 mus musculu
44	255	40.3	119	11 Q920E7	Q920E7 mus musculu
45	254	40.1	146	11 Q924Q3	Q924Q3 mus musculu

ALIGNMENTS

RESULT 1

Q9UL96 PRELIMINARY; PRT; 121 AA.
ID Q9UL96
AC Q9UL96;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Meire P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035018; AAD56254.1; -
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;
Query Match 74.4%; Score 471; DB 4; Length 121;
Best Local Similarity 73.6%; Pred. No. 1.6e-44;
Matches 89; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

OY 1 QVTLKESGPGILQPSQTLSLTCGFSGLSTSGMGVSHIROPSKGLGLAHYIWDKDKR 60
DB 1 QVTLKESGPGILVKTQTLTCTCFSGFSGLTSGMDVGWIRPPKALEWMLAIYWDKDKR 60

```
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYGCGTSVTVS 120
DB 61 YPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYGCGTSVTVS 120
QY 121 S 121
DB 121 S 121

RESULT 2
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC 099NG4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
PLasmid PHEN1.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
MEDLINE=98169018; PubMed=9510199;
RA Hawilisch H., Frank R., Hennecke M., Beensche M., Sohns B., Arseniev L.,
Beutsch W., Kola A., Kios A., Koehl J.;
Site-directed C3a-Receptor Antibodies from Phage Display Libraries.";
RT J Immunol. 160:2947-2958(1998).
DR EMBL: AJ222590; CAI10890.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1Ike.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_1Ike; 1.
KW Plasmid.
FT NON_TER.
FT NON_TER.
SQ SEQUENCE 121 AA; 13255 MW; D293E4B8C59D5B CRC64;

Query Match 63.0%; Score 398.5; DB 11; Length 121;
Best Local Similarity 64.8%; Pred. No. 1,7e-36;
Matches 79; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

DB 1 QVTLKESGPGIILQPSQTLSTLTCFSGFSLSTSGMGVSWIRPGSKGLEWLAHIYMDDDR 60
1 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYGCGTSVTVS 119
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYGCGTSVTVS 119
DB 59 YHSLKSLRSLTISKDNKSKSVFLKLSQTEDTATYYCARRVYKANYAMDYWGCGTSVTV 118
QY 120 SS 121
DB 119 SS 120

RESULT 3
Q91X92 PRELIMINARY; PRT; 482 AA.
AC 091X92;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown (protein for MGC:18822).
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011181; AAH11181.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 482 AA; 51865 MW; 312E01P9C1BC7F3C CRC64;

Query Match 58.5%; Score 370.5; DB 11; Length 482;
Best Local Similarity 61.2%; Pred. No. 1,4e-32;
Matches 74; Conservative 17; Mismatches 27; Indels 3; Gaps 2;

QY 1 QVTLKESGPGIILQPSQTLSTLTCFSGFSLSTSGMGVSWIRPGSKGLEWLAHIYMDDDR 60
DB 20 QVTLKESGPGIILQPSQTLSTLTCFSGFSLSTSGMGVSWIRPGSKGLEWLAHIYMDDDR 77
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYGCGTSVTVS 120
DB 78 YNPSLKSRLTISKDNKSKSVFLKLSQTEDTATYYCARRVYKANYAMDYWGCGTSVTVS 136
QY 121 S 121
DB 137 S 137

RESULT 4
Q96KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 53.4 kDa protein.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC016369; AAH16369.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 57.1%; Score 361.5; DB 4; Length 496;
Best Local Similarity 59.2%; Pred. No. 1,4e-31;
Matches 74; Conservative 17; Mismatches 29; Indels 5; Gaps 2;

QY 1 QVTLKESGPGIILQPSQTLSTLTCFSGFSLSTSGMGVSWIRPGSKGLEWLAHIYMDDDR 60
DB 20 QVTLKESGPGIILQPSQTLSTLTCFSGFSLSTSGMGVSWIRPGSKGLEWLAHIYMDDDR 79
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR---RVSLTAYAMDYGCGTS 116
DB 80 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR---RVSLTAYAMDYGCGTS 138
QY 117 VTVSS 121
DB 139 VTVSS 143

RESULT 5
Q9UL73 PRELIMINARY; PRT; 119 AA.
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AC Q9UL73;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035041; AAD56277.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1 119
FT 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;

Query Match 57.0%; Score 361; DB 4; Length 119;
Best Local Similarity 58.7%; Pred. No. 2,4e-32;
Matches 71; Conservative 16; Mismatches 32; Indels 2; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSEFSGFLSTSGMGVSWIRPQSGGLEMLAHYWDKRR 60
DB 1 QVQLOESGPGILVKEPSETLSTCTVSGSGISSTY--SWIRPQSGGLEMLAHYWDKRR 58
QY 61 YNPSLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQSTVTV 120
DB 59 YTPSLKSRVTVISVDKSKNQFSLKLTSLTAADTAIVFCARLSMGFYEDYWGQSTLVTV 118
QY 121 S 121
DB 119 S 119

RESULT 6
Q43234 PRELIMINARY; PRT; 97 AA.
ID 043234;
AC 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rheumatoid factor RF-ET13 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Borretzen M., Natvig J.B., Thompson K.M.;
RT "Heterogenous RF structures between and within healthy individuals are
RT not related to HLA DRB1*0401".
RL Mol. Immunol. 0:0-0(1997).
DR EMBL: AF035802; AAB8534.1; -.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1 97
FT 97
SQ SEQUENCE 97 AA; 10748 MW; DDC0BFA7B9AA812D CRC64;

Query Match 56.2%; Score 356; DB 4; Length 97;
Best Local Similarity 68.0%; Pred. No. 6,6e-32;
Matches 66; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 3 TLKESGPGILQPSQTLSTLCSEFSGFLSTSGMGVSWIRPQSGGLEMLAHYWDKRR 62
DB 1 TLKESGPGILVKEPSETLSTCTVSGSGISSTY--SWIRPQSGGLEMLAHYWDKRR 60
QY 63 YNPSLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQSTVTV 119
DB 61 YTPSLKSRVTVISVDKSKNQFSLKLTSLTAADTAIVFCARLSMGFYEDYWGQSTLVTV 118
QY 120 SS 121
DB 138 SS 139

RESULT 7
Q96EY0 PRELIMINARY; PRT; 613 AA.
ID Q96EY0;
AC Q96EY0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-B-CELL;
RA Strausberg R.;
RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: BC011857; AAH11857.1; -.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; 1g; 5.
DR SMART: SM00408; 1g; 2.
DR PROSITE: PS00290; 1g; MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67273 MW; 31214203F8421E7 CRC64;

Query Match 56.0%; Score 354.5; DB 4; Length 613;
Best Local Similarity 59.0%; Pred. No. 1.1e-30;
Matches 72; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLCSEFSGFLSTSGMGVSWIRPQSGGLEMLAHYWDKRR 60
DB 20 QVQLOESGPGILVKEPSETLSTCTVSGSGISSTY--SWIRPQSGGLEMLAHYWDKRR 58
QY 61 YNPSLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQSTVTV 119
DB 78 YNPSLSKRVTVISVDKSKNQFSLKLTSLTAADTAIVFCARLSMGFYEDYWGQSTLVTV 118
QY 120 SS 121
DB 138 SS 139

RESULT 8
Q99M22 PRELIMINARY; PRT; 479 AA.
ID Q99M22;
AC Q99M22;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RT Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: BC002091; AAH02091.1; -.

